GENETICS OF HEALTH AND FERTILITY IN DAIRY CATTLE

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For

Mum and Dad

Abstract

In this study genetic parameters were estimated and the importance of genotype by feeding system interactions investigated for a range of health and fertility traits in dairy cattle. Data were from the Langhill Dairy Cattle Research Centre and two UK recording schemes, one a recording scheme operated by the Scottish Livestock Services Ltd. (SLS) and the other a health and fertility recording and management system, the Dairy Information System (DAISY).

Genetic parameters for 305 day yield of milk and its components, health traits (mastitis, somatic cell counts (SCC), lameness and milk fever) and fertility traits (calving interval, days to first service and conception to first service) were estimated using data from DAISY and SLS. Heritabilities and correlations agreed well between the two data sets implying that the nature of the recording scheme had little effect on the parameter estimates obtained. Heritabilities for all health and fertility traits were less than 0.10 with the exception of SCC which had a heritability of 0.15. The genetic correlation between SCC and mastitis was estimated to be 0.65. Genetic correlations of health and fertility traits with production were in all cases unfavourable. Using these estimates, a breeding programme designed to maximise response in production was predicted to increase calving intervals, mastitis and lameness by 0.39, 0.27 and 0.13 genetic standard deviations per unit selection differential. Restricting these traits to zero genetic change was predicted to result in 11% less overall economic response in production than an unrestricted index.

Genotype by feeding system interactions were investigated for a wider range of health and fertility traits using data from Langhill. Selection and control line animals housed and managed as one herd were assigned to either a high concentrate or low concentrate feeding system. There were no significant genetic line by feeding system interactions. However, regressions of the traits on pedigree index for fat plus protein yield (PI) were significantly different from zero for six measures of fertility and mastitis.

It was concluded that selection for production has led to a deterioration in some health and fertility traits in UK dairy herds. This deterioration could be halted, or the situation improved by direct recording and selection. However, in the absence of a national recording scheme for health and fertility, an alternative would be use predictor traits, as they are generally easier to measure and record and have higher heritabilities. Results from this study supports the use of SCC as a selection criterion for mastitis (on a small data set), but the regressions on sire predicted transmitting abilities for type were less conclusive. Therefore future research should investigate associations between health, fertility, production, type, SCC and other potential predictor traits more fully and compare the role of direct measurements of these traits or indirect predictions of them in national indices.

Declaration

I declare that this thesis is my own composition. I am the senior author of publications arising from this thesis. I wrote the manuscripts and conducted the analyses.

Jennie E. Pryce

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Publications

Refereed publications

Pryce, J.E., Esslemont, R.J., Thompson, R., Veerkamp, R.F., Kossaibati., M.A. and Simm, G. 1997. Estimation of genetic parameters using health, fertility and production data from a management recording system for dairy cattle. Animal Science (In press; based on Chapter 3).

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Conference papers

Nielsen, B.L., Veerkamp, R.F., Pryce, J.E., Simm, G. and Oldham, J.D. 1997. Effects of genotype and lactation number on health and reproductive problems in dairy cows. Proceedings of the 1997 British Society of Animal Science Winter Meeting, Paper 143.

Pryce, J.E., Simm, G., Veerkamp, R.F., Thompson, R. and Hill, W.G. 1997. Genetic and phenotypic parameter estimates of common health disorders and fertility traits in Scottish Holstein Friesian dairy cattle. Proceedings of the 1997 British Society of Animal Science Winter Meeting, Paper 24.

Pryce, J.E., Veerkamp, R.F., Esslemont, R.J., Kossaibati, M.A., and Simm G. 1997. Genetic associations amongst health and fertility traits for two UK recording schemes. In: E. Strandberg (compiler), Proceedings International Workshop on Genetic Improvement of Functional Traits in Cattle, Uppsala, Sweden, Interbull bulletin 15.

Pryce, J.E., Veerkamp, R.F. and Simm, G. 1998. Expected correlated responses in health and fertility traits to selection on production in dairy cattle. Proceedings of the 6th World Congress in Genetics Applied to Livestock Production, Armidale, Australia, January 1998. Vol. 23: 383-386.

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Abbreviations

AI:	Artificial insemination
AM:	Animal model
b:	Regression coefficient
c^2:	Permanent environmental effect
C:	Control line
CI:	Calving interval
CON:	Interval from calving to conception
CV_a:	Coefficient of genetic variation
DAISY:	Dairy Information System
DFH:	Days to first heat
DFS:	Days to first service
DOP:	Days open
FSC:	Conception to first service
GLMM:	Generalised Linear Mixed Models
h^2:	Heritability
HC:	High concentrate
HFS:	Holstein Friesian Society of Great Britain and Ireland
IFL:	Interval from first to last insemination
LAME:	Lameness
LC:	Low concentrate
LM:	Linear model
MACE:	Multiple-trait Across Country Evaluations
MAST:	Mastitis
MFEV:	Milk fever
NR:	Non-return
ONO:	Oestrus not observed
PI:	Pedigree index
r_g:	Genetic correlation
r_p:	Phenotypic correlation
REML:	Restricted maximum likelihood
s.d.:	Standard deviation
s.e.:	Standard error
S:	Selection line
SAC:	Scottish Agricultural College
SCC:	Somatic cell count
SCS:	Somatic cell score
SM:	Sire model
SLS:	Scottish Livestock Services Ltd.
SPC:	Number of services per conception
t:	Tonne
TM:	Threshold model
VCE:	Variance Components and Estimation
σ_p:	Phenotypic standard deviation

Introduction

The ultimate aim of most dairy producers is to maximise profitability. While yields of protein, fat and milk are the traits of greatest importance in this respect, there are several reasons why breeding goals should be broadened to include traits other than production, such as health and fertility. Firstly, it is evident that selection for milk yield alone in dairy cattle leads to a decline in fertility and an increase in the incidence of health disorders which may have consequences for welfare. As well as being ethically important to address this, it may become increasingly economically important; several dairy companies and supermarkets have already set up welfare assured production systems. Secondly, reducing health and fertility costs may help to improve direct economic efficiency which should increase dairy farm profits.

Studies on culling reasons of dairy cattle show that most cows are disposed of for involuntary reasons. For example Kossaibati and Esslemont (1995) reported that reproductive failure was the predominant culling reason in farms in southern England, accounting for 36.5% of all cows culled, with mastitis the second most important culling reason (10.1%). If the number of involuntary culls were reduced, more cattle would reach their productive peak (fourth to fifth lactation) and fewer heifers would need to be reared as replacements.

Large improvements to dairy cow health and fertility can be achieved through improvements to management and nutrition. However, selection may be a complementary, albeit longer term, way of achieving better health and fertility. Longevity has already been included as part of the breeding goal in a UK selection index for total economic merit (ITEM; Veerkamp *et al.*, 1995a).

In Scandinavia some health and fertility traits are already included as breeding objectives in breeding programmes, to counter the deterioration in health and fertility due to selection for increased milk yields (e.g. Solbu and Lie, 1990; Eriksson and

Wretler, 1991; Philipsson *et al.*, 1994). This is possible as all veterinary treatments are compulsorily recorded and stored in a central database in Sweden, Norway, Denmark and Finland (Forshell *et al.*, 1995). Inclusion of health and fertility traits elsewhere in the world has been limited by a lack of reliable data.

Several dairy recording services in the UK now offer comprehensive recording of health, fertility and culling information. However, only recently has sufficient data been accumulated for a genetic analysis. The main aim of this thesis was to investigate the genetics of health and fertility traits for the UK situation.

Chapter 1 is a general review of recent heritability estimates of health and fertility traits, and correlations with milk production traits. In addition to this, the potential use of several alternative selection criteria (for health and fertility) are discussed, such as somatic cell counts and linear type scores. Genetic parameter estimates for health and fertility traits, estimated using data from commercial UK herds, are presented in Chapters 2 and 3. The data used for these studies were from two recording schemes with different objectives. The study reported in Chapter 2 includes estimates from the Scottish Livestock Services (SLS), which is the main milk recording scheme in Scotland. Although SLS data for health and fertility is limited in terms of recording detail, large numbers of records (from over 400 herds) have been collected since the start of the scheme in 1994. There is no charge for the SLS scheme. The study reported in Chapter 3 includes estimates obtained using data from a recording scheme operated by the University of Reading / National Milk Records known as the Dairy Information System (DAISY). This scheme was designed specifically for recording health and fertility data. DAISY is computer based and participants pay for software to record this type of information. One of the aims of this thesis was to determine whether parameter estimates from recording schemes differ.

In the study reported in Chapter 4, the consequences of selection for butterfat plus protein yield on various health and fertility traits were investigated. It has been

suggested that preferential treatment of high yielding cows and selection for other traits (such as type) may affect correlations between milk production and health and fertility traits. Some of these problems are avoided when data from research farms are used, such as the Langhill Dairy Cattle Research Centre, where cows are fed and managed in the same way regardless of genotype. Cows from Langhill are divided into two genetic groups; a selection line (S) where sires are selected for high genetic merit for fat and protein yield and a control line (C; UK average genetic merit). Cows from each genetic group are fed either a high concentrate (HC) or low concentrate (LC) diet. The importance of genotype by environment interactions for health and fertility traits was investigated by examining the performance of S and C lines on HC and LC diets.

In the study reported in Chapter 5, the genetic parameters estimated for SLS and DAISY (Chapters 2 and 3) were used to i) predict correlated responses in calving interval, mastitis and lameness, when selection was for production only and ii) predict responses when calving interval, mastitis and lameness are restricted to zero genetic change. Finally, the potential use of somatic cell count as a selection criteria for mastitis was investigated.

Chapter 6 is a discussion of the main points raised in each of the other chapters in the context of future UK breeding goals. Particular emphasis is placed on: i) methods of recording health and fertility; ii) the relationship between these traits and milk yield iii) appropriate selection criteria for traits chosen as future selection objectives for the UK.

Chapter 1

Genetics of health and fertility in dairy cattle - a review

1.1 Introduction

The manifestation of health disorders and infertility can be attributed to management and environmental factors. However, there is evidence in the literature to suggest that some of these traits also have a genetic component. Selection solely for milk and its components appears to have led to a deterioration in some aspects of health and fertility. Improving nutrition, housing and hygiene etc. should be considered as the best short-term strategies for reducing infertility and the incidence of health disorders, while selection may be a better long-term strategy. In this chapter recent literature relating to the genetics of these traits is reviewed.

Health disorders are usually classified as occurring (or not) within a lactation. Similarly, whether a cow has conceived after a service event is often used as a measure of fertility. Thus, most health disorders and some fertility traits are considered to be all-or-none (0/1) traits. It is often assumed that 0/1 traits have an underlying continuous distribution. This is a reasonable assumption since it is believed that many 0/1 traits are under the control of the combined effects of several genes and the environment and that there is an underlying distribution of liability (Falconer, 1989). There are two main approaches used to analyse 0/1 data: either i) a linear model (LM) which would ignore the binary nature of the data; or ii) a threshold model (TM) and assume that the observed result depends on the value of the underlying continuous normal variable exceeding a threshold, heritabilities estimated using this method are on the assumed underlying scale.

However, although either model may be equally suitable for parameter estimation, the heritability estimates obtained are not directly comparable. Furthermore as the heritability is affected by the incidence, estimates obtained using an LM (where

incidences in populations or sub-populations differ) cannot be compared to each other without adjusting for the incidence. Thus it is necessary to convert the estimate to the hypothetical underlying scale (h^2_L) using the transformation proposed by Robertson and Lerner (1949):

$$h^2_L = h^2_{01} * \frac{p(1-p)}{z^2} \qquad \text{equation1.1}$$

where h^2_{01} is the heritability estimate on the binomial scale, p is the proportional incidence of the trait (frequency of 1's), z is the height of the ordinate of a standardised normal at the threshold corresponding to p.

1.2 Fertility

1.2.1 Definition of fertility

Conception and maintenance of pregnancy in dairy cattle involves a synchrony between management effects and physiological processes (controlled by hormones). These include adequate heat detection; timing of insemination; production of an ovum capable of being fertilised and a uterus capable of supporting pregnancy. It is apparent, however, that some or all of these processes are operating sub-optimally. In the UK culling for failure to conceive accounts for around 37% of all culls (Esslemont and Kossaibati, 1997).

Service and calving dates are recorded by most milk recording agencies as this information is needed by farms for management purposes and to provide parentage details for the resulting offspring. Fertility measures calculated from these dates are widely used to give an indication of the fertility performance of herds and individual animals. Furthermore, these measures are generally used in studies where the genetic control of cow fertility is investigated.

Fertility measures calculated from calving and service dates can be divided into two categories: i) fertility scores which are categorical and ii) interval traits, which

include measures based on the length of time between one event and another. Some common measures of female fertility are presented in Table 1.1.

Table 1.1 Commonly used measures of fertility and abbreviations

Measure of fertility	Abbreviation
Fertility scores:	
[1]Non-return after first insemination	NR
Conception to first service	FSC
Number of services per conception	SPC
Interval traits:	
Calving interval	CI
Days open	DOP
Days to first service	DFS
Interval from first to last insemination	IFL

[1]Non-return traits are commonly used where the outcome of an insemination is unknown and it is assumed that the first insemination has resulted in conception if there are no others recorded within a certain number of days e.g. non-return after 56 days is commonly used.

Fertility scores are generally considered to be the most useful measures of female fertility. One outcome of an improvement in these traits is that fewer straws of semen are required per conception. In some countries maintaining short calving intervals is also important. In New Zealand, for example, production and reproduction are essentially matched to the growth rate patterns of grass, which is reflected by average calving intervals of 365 days (Grosshans *et al.,* 1997). In countries where cow diets are less dependent on fresh grass there is less pressure to maintain short calving intervals, for example in most of Europe and North America, the average tends to be around 380 days (e.g. Ouweltjes *et al.,* 1996b; Kossaibati and Esslemont, 1995).

Measures of days open, calving interval and to some extent conception to first service may produce biased parameter estimates, as they do not include cows that are culled because of fertility problems. Non-return rate has been suggested as a better measure of fertility (e.g. De Jong, 1995), as it is believed to be less affected by the farmer than interval traits, more data are generally available than for conception to first service (as there is no requirement for two consecutive calving dates) and the outcome (a greater probability of conception to first service) is desirable. However, using a non-return trait as a measure of fertility may also lead to biased estimates. For example, if a cow is not re-inseminated this does not necessarily mean she is in calf, as the farmer may have made a decision to cull that cow subsequent to the first

insemination. Another limitation is when stock bulls are used in addition to AI, as natural service dates may not be recorded. Where incomplete service records are available, conception to first service may be a more suitable measure. Conception can be determined by either i) a subsequent calving date, or ii) pregnancy diagnosis, which although expensive is routinely practised in some countries (e.g. Israel; Weller and Ron, 1992).

It can be concluded that none of the measures of fertility described in this review are without bias, as service and subsequent conception are influenced by both management decisions and the biological potential of the animal. However, in most temperate countries, fertility scores seem to be the best of these measures. In practical breeding programmes, the choice of fertility score is affected by the integrity of the data. Analysis of non-return rates would produce biased estimates if a large number of inseminations are not recorded. In this situation conception to first service may be a better choice.

1.2.2 Heritability estimates for fertility traits

Most genetic analyses of fertility adjust for herd, year, season (or month) and age effects (Jansen, 1985). In addition, many adjust for the effect of the service sire and technician. There is also some indication of a potential genotype by environment interaction for some fertility traits. Using data from seven research herds in North Carolina, Faust *et al.* (1989) observed that sire groups ranked differently for all reproductive measures in warmer calving seasons than cooler seasons. In a review article, Jansen (1985) reported two studies where a sire by herd-year-season interaction had been found.

Recent heritability estimates and coefficients of genetic variation (CV_a) for some common fertility measures are presented in Table 1.2. Differences between estimates may be attributed to several causes including the breed of cattle, data editing procedure, the type of model fitted and the nature of the recording system. Swalve *et al.* (1992) compared heritability estimates obtained using the same model, but data

from a conventional (paper) recording system and an electronic recording system. Although heritability estimates were slightly higher for electronic recording, all differences between systems for all fertility traits were non-significant.

Table 1.2 Heritability estimates (x 100) for some common measures of fertility in lactating cows

[1]Trait	[2]Heritability (x 100) in lactation			[3]CV_a	[4]Model	Breed	Cows (sires)	Source
	1	2	all					
CI	4			3	LM, SM	Holstein	22791 (2548)	Dadati *et al.* (1986)
DFS	5.8			-	LM, SM			Faust *et al.* (1989)
FSC	3.2			-				
SPC	8.4			-				
FSC	5 (0.01)			18	LM, SM			Oltenacu *et al.* (1991)
SPC	5 (0.01)			13				
DFS			2.9	5	LM, SM	Holstein	235589 (306)	Hayes *et al.* (1992)
DOP			4.7	11				
SPC			2.8	10				
DOP	1			4	LM, SM	Ayrshire	8156 (65)	Moore *et al.* (1992)
DOP	3			8		Holstein	80604 (410)	
SPC	0.6 (0.2)	1.2 (0.3)		5	LM, SM	Holstein	57972 (308)	Swalve *et al.* (1992)
IFL	1.0 (0.3)	1.1 (0.3)		17				
NR56	0.4 (0.3)	0.8 (0.3)		4				
NR90	0.7 (0.2)	0.7 (0.4)		6				
DFS	5	7		6	LM, SM	Holstein	6699 (214)	Van Arendonk *et al.* (1992)
DOP	1	1		4				
SPC		4		9				
NR56		3		11				
FSC			1.2		TM, SM	Holstein	131486 (228)	Weller and Ron (1992)
DFS	3 (0)	3 (1)		6	LM, SM	Holstein	168831 (629)	Bagnato and Oltenacu (1993)
DOP	3 (0)	2 (0)		7				
FSC	1 (0)	1 (0)		6				
SPC	1 (0)	1 (0)		6				
FSC	2.2		1.9	3	LM, SM	Holstein	250215 (1128)	Boichard and Manfredi (1994)
FSC	3.4				TM, SM			
CI	9.8			6	LM, AM	Holstein	3195	Campos *et al.* (1994)
DOP	5.2			14			4041	
CI	2.1			3		Jersey	1131	
DOP	2.6			10			2143	
CI	3 (2)			2	LM, SM	Holstein	82659 (1456)	Hoekstra *et al.* (1994)
DFS	4 (2)			9				
IFL	2 (2)			23				
NR56	4 (2)			6				
FSC	5 (2)			8				
IFL			3.8 (1.2)	30	LM, SM	Swiss	706040 (1681)	Hodel *et al.* (1995)
NR90			2.1 (0.8)	11		Simmental		
DFS	7.0			-	LM, SM		2687493	Pedersen and Jensen (1996)
IFL	2.0			-				
NR56	1.0			-				
CI	1.7 (0.4)	0.6 (0.3)		-	LM, AM	Holstein	66294	Grosshans *et al.* (1997)
DFS	5.8 (0.6)	6.4 (0.8)		21		and		
IFL	1.2 (0.3)	1 (0.3)		17		Jersey		
DOP	2.3 (0.4)	0.6 (0.3)		4				
SPC	0.7 (0.5)	1.0 (0.3)		5				
NR21	3.7 (0.5)			17				
NR42	2.9 (0.4)			9				

[1]Trait: CI, calving interval; DFS, days to first service; DOP days open; IFL, interval first to last insemination; FSC conception to first service; SPC, number of services per conception; NR56, non-return 56 days

[2]Heritability in each lactation x 100 (s.e.)

[3]CV_a: Coefficient of genetic variation x 100, the genetic standard deviation divided by the phenotypic mean

[4]Model: LM, Linear model; TM, threshold model; SM, sire model; AM, animal model

Heritability estimates for fertility traits were small, typically less than 10%. However the genetic variation of some traits seems substantial. Table 1.3 includes a summary of simple means of heritability and CV_a estimates for each trait from the studies in Table 1.2.

Table 1.3 Simple means of heritability estimates (x 100) and genetic coefficients of variation (x 100) from 15 studies

[1]Trait	Heritability (mean)	CV_a (mean)	Number of studies
CI	3.5	4	4
DFS	5.0	9	7
DOP	2.4	8	6
IFL	1.7	22	5
NR	1.9	9	6
FSC	2.7	11	5
SPC	2.6	8	7
Mean of all traits	2.8	10	

[1]Trait: CI, calving interval; DFS, days to first service; DOP days open; IFL, interval first to last insemination; NR, non-return; FSC conception to first service; SPC, number of services per conception.

The coefficient of genetic variation (CV_a) is the genetic standard deviation as a percentage of the phenotypic mean. The largest mean CV_a is for the interval from first to last inseminations which is 22. The overall mean for all traits is 10, which is comparable to the CV_a for production traits, e.g. Grosshans *et al.* (1997) reported values of 9, 7 and 7 for CV_a estimates of milk, fat and protein yields. However, the phenotypic distribution of fertility data is often skewed which may lead to an overestimation of the standard deviation. Philipsson (1981) suggested that studies of progeny group estimated breeding values may give a better indication of the true genetic variation. Using two data sets of sire relative breeding values for 'female fertility' in Swedish Friesian (SLB) and Swedish Red (SRB) breeds, he estimated that coefficients of variation for the two respective breeds were 7 and 8, which are 20% to 30% smaller than the estimates in Table 1.3.

Most genetic correlations between fertility score traits approach unity. For example, the genetic correlation between number of services per conception and conception to first service was estimated to be -0.98 (Bagnato and Oltenacu, 1993) and that between non-return after 56 days and conception to first service was estimated to be

between 0.86 and 0.93 (Hoekstra *et al.,* 1994; De Jong, 1995). Genetic correlations between interval traits are also high, e.g. between calving interval, days to first service and days open estimates are commonly greater than 0.7 (Bagnato and Oltenacu, 1993; Hoekstra *et al.,* 1994 and Grosshans *et al.,* 1997). Correlations between interval traits and fertility scores are generally smaller, ranging between 0.4 and 0.6 (Bagnato and Oltenacu, 1993; Hoekstra *et al.,* 1994 and Grosshans *et al.,* 1997). High genetic correlations between most of these traits is expected, as many are very closely related measures, for example calving interval is simply days open plus the gestation length.

Most of the heritability estimates presented in Table 1.2 were for fertility in first lactation animals. Some authors have also considered correlations between age groups. Bagnato and Oltenacu (1993) obtained high genetic correlation estimates between the same traits in different lactations (0.49 to 0.99). Of particular use would be if fertility records from maiden heifers could be used to predict fertility in lactating animals, as these records would obviously be available earlier and could be used for progeny testing. Several studies have investigated the relationship between maiden heifer and cow fertility. Oltenacu *et al.* (1991) obtained genetic correlations between maiden heifer and first lactation fertility, of around 0.9 for SRB and 0.6 to 0.7 for SLB breeds. Pedersen and Jensen (1995) also estimated moderate genetic correlations of 0.3 to 0.5 and suggested that heifer data could indeed be used for progeny testing. However, Swalve *et al.* (1992) reported large differences between heritability estimates for maiden heifer and cow fertility. Both Philipsson (1981) and Nebel and McGilliard (1993) cited several other studies where estimates of correlations were contradictory. Maiden heifer fertility may reflect the true genetic potential of the animal, while cow fertility may be affected by factors such as lactation effects and metabolic load.

Heritability estimates of around 3% are typical for fertility traits. It is not surprising that heritabilities are low as reproductive success is affected by decision policies, such as when to resume inseminations after calving, timing of service, strategies of

oestrus detection etc. Despite this, most measures of fertility seem to have substantial genetic variation, making genetic progress in some of these traits feasible. However, because of low heritabilities, large progeny groups would be required to get accurate estimated breeding values. For example when the heritability is assumed to be 0.03 a progeny group size of 200 would yield an accuracy of ~0.85.

1.2.3 The relationship between milk production and fertility

There is evidence to suggest that single trait selection for production has led to a deterioration in fertility. Table 1.4 gives recent estimates for the genetic and phenotypic correlations between production and fertility measures in first lactation cows.

Table 1.4 Estimates of genetic correlations between fertility and milk production traits in first lactation cows

	305d milk		100d milk		305d fat		305d protein		
[1]Trait	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p	Source
CI	[3]0.55	[4]0.18			0.41	0.15	0.62	0.18	Hoekstra *et al.* (1994)
	0.17	-			0.20	-	0.11	-	Campos *et al.* (1994)
	0.22	0.03			0.03	0.02	0.07	0.03	Grosshans *et al.* (1997)
DFS	0.22	0.11	0.42	0.07	0.51	0.10	0.38	0.05	Van Arendonk *et al.* (1989)
	0.39	0.11							Bagnato and Oltenacu (1993)
	0.44	0.12			0.39	0.10	0.41	0.11	Hoekstra *et al.* (1994)
	0.25	-0.00			-0.13	-0.04	-0.17	-0.04	Grosshans *et al.* (1997)
DOP	0.64	0.11	0.81	0.17	0.95	0.19	1.02	0.19	Van Arendonk *et al.* (1989)
	0.36	0.12							Bagnato and Oltenacu (1993)
	0.16	-			0.22	-	0.14	-	Campos *et al.* (1994)
	0.25	0.01			0.04	-0.01	0.04	-0.01	Grosshans *et al.* (1997)
FSC	-0.21	-0.08							Bagnato and Oltenacu (1993)
			-0.62	-0.03					Boichard and Manfredi (1994)
	-0.24	-0.10			-0.24	-0.08	-0.38	-0.11	Hoekstra *et al.* (1994)

[1]Trait: CI, calving interval; DFS, days to first service; DOP days open; FSC conception to first service.
[2]305d milk: Yield of milk over 305 days

Most genetic correlations between fertility and production presented in Table 1.4 are unfavourable. The only exception is the relationship between DFS and fat and protein yields reported by Grosshans *et al.* (1997). Although Table 1.4 only includes correlation estimates for first lactation cattle, several authors have investigated the relationship between production and fertility in other lactations. Bagnato and Oltenacu (1993) obtained high genetic correlations between production in the first parity and fertility measures in later parities, indicating that selection for high

production in first lactation cattle would result in a deterioration of fertility in later lactations. Van Arendonk *et al.* (1989) reported that correlations between 305 day milk yield and fertility were very similar in first and second lactation cattle, although the correlations were slightly smaller between fertility and 100 day milk yield in second lactation cattle.

Philipsson (1981) argued that the most reliable measures of the relationship between production and fertility is with production in the early part of the lactation, as production beyond seven to eight months after calving are likely to be influenced by the time of conception, as cows may be at very different stages of gestation. Most genetic correlations are higher between fertility and 100 day production than 305 day production (Table 1.4). The explanation for this could be that production is fuelled by progressively greater losses of body condition rather than higher food intake. This is a particular problem in high yielding cows that often cannot maintain a positive energy balance i.e. consume enough energy to maintain yield requirements (Nebel and McGilliard, 1993), especially in early lactation.

Some authors have suggested that energy corrected milk yield should be used in preference to other production measures in studies investigating the relationship between yield and fertility, as it is believed to be a better measure of milk energy output. Oltenacu *et al.* (1991) investigated the relationship between conception to first service and fat corrected milk yield (FCM) in the first 100 days and obtained genetic correlations of -0.13 and -0.32 for Swedish Red and Swedish Black and White breeds respectively. Van Arendonk *et al.* (1989) used fat and protein corrected milk (FPCM), calculated using this formula: FPCM=0.349*MILK+10.7*FAT+6.7*PROT. They considered the relationship between fertility and this trait over 100 and 305 days. Not surprisingly, genetic correlations between fertility and FPCM seem to be between the estimates for milk and fat yields.

Marti and Funk (1993) considered days open in herds divided into four production level groups and found that the heritability of days open was higher in high producing herds. The number of days open increased with production level and the antagonism was more severe for low producing herds. They suggested that this may be because management of both production and reproduction is of a better quality in higher producing herds.

Estimates of the relationship between production and fertility from field data may be difficult to interpret owing to a confounding of management decisions with biological effects (Philipsson, 1981; Jansen, 1985). If farmers deliberately delay inseminating high producing cows, then the genetic variance would be artificially inflated. This may affect the correlations with the interval traits and, to a smaller extent, conception rate.

Table 1.5 Heritabilities (x 100) and incidences of various fertility disorders in dairy cattle

Trait	Heritability in lactation				[1]Incidence	Breed	Sires	Cows	Source
	1	2	3	all	(%)		(n)	(n)	
Retained placenta	5 (7)	9 (8)			6.4	Holstein		[2]1722	Lin *et al.* (1989)
Metritis	19 (8)	26 (9)			8.4			[2]1704	
Cystic ovaries	12 (8)	8 (8)	2 (8)		6.8			[2]1591	
Retained placenta	2.5				4.4	Holstein	190	38164	Eriksson and Wretler (1991)
Cystic ovaries	0.9				0.7	Holstein	190	38164	
Retained placenta				5	5.8	Holstein	229	9187	Lyons *et al.* (1991)
Cystic ovaries				5	7.9	Holstein	229	9187	
Fertility disorders				0.8	1.8	Holstein	117	9516	Koenen *et al.* (1994)
Cystic ovaries	13			8	8.3	Holstein	148	4640	Uribe *et al.* (1995)
Ovulatory disorder	1.2 (0.4)	1.9 (0.5)	0.9 (0.7)		10.9	Ayrshire	538	23196	Poso and Mantysaari (1996a)
Metritis	0.6 (0.4)	0.7 (0.4)	0.6 (0.6)		2.7				
Retained placenta				4 (1)	6.3	Holstein	66	4590	[3,4]Ouweltjes *et al.* (1996a)
Metritis				4 (1)	17.8				(Data set 1)
Oestrus not observed				5 (2)	56.6				
Retained placenta				1 (1)	8.6	Holstein	78	2503	(Data set 2)
Metritis				3 (1)	9.4				
Reproductive disorders	2 (0.2)	1 (0.2)	2 (0.3)		14	Holstein		[2]163361	Nielsen *et al.* (1997a)
Reproductive disorders	2 (0.4)	2 (0.4)	2 (0.5)		15	Red Danish		[2]58259	
Reproductive disorders	0.2 (0.1)	1 (0.2)	1 (0.4)		6	Danish Jersey		[2]31559	

[1]Incidence, where more than one lactation was analysed, the incidence is the mean over lactations
[2]Number of first lactation records
[3]Parameter estimates were from two recording schemes in Holland
[4]Ouweltjes *et al.* (1996a) used a linear animal model, all other analyses were with linear sire models

1.2.4 Breeding for a reduced incidence of reproductive problems

Reproductive problems include retained placentas, metritis, cystic ovaries, failure to rebreed and others of lesser importance. Many of these disorders arise from problems occurring at parturition and may result in a prolonged period to first service thus affecting common measures for fertility calculated from calving and service dates (Philipsson, 1981). Heritability estimates for various reproductive disorders are given in Table 1.5. These are generally low, although Lin *et al.* (1989) obtained relatively high estimates which seemed to decrease with age. It is difficult to ascertain whether there is a similar trend in the other studies, as heritability estimates are much lower. If heritabilities do indeed decrease with age, then it may mean that genetic evaluation of first lactation records might be sufficient for selection, although this would require reasonably high correlations between lactations for these traits.

Most authors cited in this review did not investigate relationships between reproductive disorders and measures of fertility calculated from service information. However, one exception was the study of Poso and Mantysaari (1996a). They obtained a high genetic correlation between operational days open and ovulatory disorders (0.80), which they interpreted as meaning that these are different measures of the same trait. However the correlation between operational days open and metritis was smaller (0.37).

1.3 Mastitis

1.3.1 Definition of mastitis

Mastitis is an inflammation of the udder tissue caused by one or more of a number of organisms which gain access through the teat orifice. The causative bacteria of mastitis can be categorised as major and minor pathogens. The most common major pathogens include *Staphylococcus aureus*, *Streptococcus agalactiae*, and coliforms, streptococci, and enterococci of environmental origin. Major pathogens have the greatest economic impact and are responsible for an associated increase in somatic cell count (Harmon, 1994). The initial stages are subclinical with no visual effect on the udder although milk yield is reduced and bacteria are present in the secretion.

Clinical mastitis is characterised by reduced milk yield and clots in the milk caused by precipitation of milk proteins. Severe cases of mastitis may be accompanied by an elevated temperature.

Mastitis is a costly disease, in addition to treatment costs, there are costs associated with staff time, discarded milk, a reduction in milk yield for the remainder of the lactation and an increased risk of culling and fatality. Taking these costs into consideration, Kossaibati and Esslemont (1997) estimated that the average total cost of mild mastitis in a lactation would be £98 (assuming an average of 1.6 cases per lactation). Severe and fatal cases were estimated to cost, on average, £433 and £2214 per lactation. This estimate for a fatal case of mastitis seems quite high, but includes the cull price of a cow and replacement costs. If the overall prevalence of mild, severe and fatal are 70%, 29% and 1% respectively, then the total cost per average affected cow would be £218. Eriksson (1991) used literature estimates and similar assumptions to Kossaibati and Esslemont (1995) to calculate the economic value of mastitis in the USA, Denmark and Sweden. He estimated that a single case of mastitis would be worth approximately 130 kg of milk per cow in Denmark and the USA and 430 kg of milk in Sweden. Assuming a milk price of £0.20 per kg of milk in the UK, these would be equivalent to £26 and £86. These differ quite substantially from the overall mean of £218 obtained by Kossaibati and Esslemont (1995). There are clearly differences in veterinary and other costs between countries, as highlighted by Eriksson (1991) and the use of slightly different assumptions may affect the derivation of economic values for traits where the associated costs arise from many different causes.

1.3.2 Heritability estimates for clinical mastitis

In a very comprehensive review of production diseases, Emanuelson (1988) reported heritability estimates for mastitis ranging between 0.00 and 0.37 with a mean of 0.07. Table 1.6 includes heritability estimates (x100), subsequent to Emanuelson's study.

Table 1.6 Heritability estimates (x100) for mastitis

[1]Herit (x100)	[2]Incid (%)	Lact	[3]Breed	[4]Country	[5]Model	Sires (n)	Records (n)	Source
2	7.5	1	SRB	Sweden	LM, SM	379	102525	Eriksson and Wretler (1991)
2	10.8	1	SLB		LM, SM	190	38164	
14	34.1	all	Holstein	USA	LM, SM	229	9187	Lyons *et al.* (1991)
8.8	10.5	1		Norway	TM, SM	704	208693	Simianer *et al.* (1991)
1	5.1	1	Holstein	Israel	LM, SM	292	148143	Weller *et al.* (1992)
6	5.6	1	Holstein	Holland	TM, SM	224	3617	Groen *et al.* (1994)
2	5.6	1			LM, SM			
1.8	21.7	1	Holstein	Sweden	LM, SM	117	9516	Koenen *et al.* (1994)
2.5	21	1	Holstein	Denmark	LM, AM	614	4603	Lund *et al.* (1994)
1.5	12.5	1	Holstein	Canada	TM, SM	81	2639	Uribe *et al.* (1995)
0	16.7	all			TM, SM	160	5229	
2.5	5.4	1	Ayrshire	Finland	LM, SM	N.R	23167	Poso and Mantysaari (1996a)
4.6	7.9	2			LM, SM	N.R	17891	
9	26.3	1		Norway	LM, SM	257	70861	Heringstad *et al.* (1997)
5	26.3	1			TM, SM	257	70861	
2	7.8	1	Ayrshire	Finland	LM, SM	637	23854	Luttinen and Juga (1997)
2	8.1	all			LM, SM			
1	10.9	1	Holstein		LM, SM	232	10720	
1	10.9	all			LM, SM			
4	38	1	Holstein	Denmark	LM, SM		163361	[5]Nielsen *et al.* (1997a)
4	38	2			LM, SM		191557	
6	41	1	RD		LM, SM		58259	
5	42	2			LM, SM		41465	

[1]Herit: Heritability estimates
[2]Breed: SRB, Swedish Red; SLB, Swedish Friesian; RD Red Danish
[3]Country of data origin
[4]Model: LM, linear model; TM, threshold model
[5]Analysed udder diseases included summer mastitis, teat damage, mastitis etc.

Most studies in Table 1.6 were of first lactation Holstein animals. As expected, most of the larger studies (in terms of numbers of records) are from the Scandinavian countries, as recording of veterinary treatment of diseases on farm animals is compulsory. Nielsen *et al.* (1997a) analysed udder diseases which included clinical mastitis in addition to summer mastitis and teat damage, consequently the incidence is higher than other studies.

In this review, heritability estimates for mastitis range between 0 and 0.15 with a mean of 0.05. Lyons *et al.* (1991) and Uribe *et al.* (1995) estimated the heritability of mastitis using data from all lactations, and they obtained the highest and lowest heritabilities. Most other authors advocated using only first lactation records as data in subsequent lactations may be biased due to culling. However, as the incidence of mastitis is known to increase with lactation number, it is important to know whether selection for increased resistance to mastitis using first lactation records of clinical

mastitis would result in a reduced incidence of mastitis in both animals in first and later lactations. Poso and Mantysaari (1996b) obtained reasonably high correlations between mastitis in first, second and third lactations, ranging between 0.67 and 0.90.

Lyons *et al.* (1991) used data from two sources, one data set consisted of health disorders recorded on farms and the other consisted of data recorded on farms, but copied by company personnel. The estimate in Table 1.6 is a combined estimate of the two sources. The heritability estimated from the producer data was much higher (0.23) than the heritability estimated from the copied data (0.13). The authors commented that the producer data was more complete and thus more likely to be accurate. Even though both these estimates are high, compared to other estimates in Table 1.6, they differ from each other quite substantially, indicating that heritability estimates may be affected by the method of recording data.

A contentious issue in deriving heritability estimates for all-or-none traits has been whether it is appropriate to assume a normal distribution and hence use a linear model for traits that are clearly categorical (section 1.1). A good way to compare linear and threshold models is to use both models on the same data set. Heringstad *et al.* (1997) found heritability estimates of 0.05 and 0.09 for linear and threshold models respectively, on a large Norwegian data set. When the heritability estimate from the linear model is transformed to the underlying scale (using equation 1.1) the heritability is the same as that obtained from the threshold model, 0.09. Groen *et al.* (1994) obtained heritability estimates of 0.02 (0.08 on the underlying scale) for a linear model and 0.06 for a threshold model using a smaller Dutch data set. Thus heritabilities estimated using threshold models seem to be roughly double those estimated using linear models, but transformed to the underlying scale they are very similar. Heringstad *et al.* (1997) also investigated the ranking of sire estimated breeding values using the two models and found very high correlations between estimates (>0.99), indicating that selection decisions are unlikely to be affected by the choice of model used to analyse the data.

1.3.3 Somatic cell counts - a selection criterion for mastitis

There are two practical limitations of using clinical recordings of mastitis in genetic improvement schemes: i) mastitis is usually measured as an all-or-none trait within a lactation, hence there is no indication of the severity of each case and ii) estimates of heritabilities may be lower than expected due to inaccurate or incomplete field records.

A possible solution to these problems is to use information from a correlated trait. Numerous studies have indicated a positive relationship between somatic cell counts (SCC) measured in test-day milk samples and clinical cases of mastitis (for a review, see Mrode and Swanson, 1996). SCC is measured on a continuous scale, so a more objective description of the severity of mastitis may be obtained. SCC is also of economic importance in its own right. The introduction of penalty systems for high bulk tank samples of SCC has given dairy farmers an incentive to reduce herd SCCs. In the UK most milk buyers penalise farmers for high bulk tank SCC using a penalty banding system, making derivation of economic values for use in a breed improvement programme difficult (Veerkamp *et al.*, 1997).

Table 1.7 Heritability estimates (and standard errors) for log transformed somatic cell count

Heritability in lactation				[1]Breed	[2]Model	sires	cows	Source
1	2	3	all			(n)	(n)	
0.03	0.02	0.11		Holstein	TD, SM	80	3376	Heuven *et al.* (1988)
0.07	0.39	0.24	0.12		LA, SM			
(0.06)	(0.21)	(0.12)	(0.05)					
			0.11	Holstein	LA, SM	236	12616	Monardes *et al.* (1990)
0.14	0.12	0.11		Holstein	LA, SM	691	80069	Banos and Shook (1990)
(0.01)	(0.01)	(0.02)						
0.12				Holstein	LA, SM	437	16281	Rogers *et al.* (1991)
0.05	0.07	0.11	0.12	Holstein	LA, AM	334	5278	Da *et al.* (1992)
0.19			0.27	Holstein	LA, SM	215	19764	Weller *et al.* (1992)
(0.10)			(0.06)					
0.16			0.13	Holstein	LA, SM	392	5246	Welper and Freeman (1992)
0.18				Holstein	LA, AM			Lund *et al.* (1994)
(0.08)								
			0.09	Holstein	LA, AM		1135752	Schutz *et al.* (1995)
			0.07	Ayrshire			4314	
			0.07	BS			7845	
			0.11	Guernsey			18115	
			0.09	Jersey			67862	
			0.08	Shorthorn				
0.17				Holstein	LA, SDM		65491	Miglior *et al.* (1995)
0.11			0.11	Holstein	LA, AM		63414	Mrode *et al.* (1995)
(0.01)			(0.01)					
0.12			0.11	Jersey	LA, AM		14507	
(0.02)			(0.02)					
0.09			0.12	Ayrshire	LA, AM		7966	
(0.03)			(0.03)					
0.09	0.09		0.11	Holstein	TD, GIBB		392487	Reents *et al.* (1995b)
0.08	0.13		0.14	Holstein	TD, GIBB		1487279	Reents (1996)
0.12	0.15			Jersey	LA, SM			Rogers *et al.* (1995)
(0.04)	(0.03)							
0.16	0.18	0.17		Ayrshire	LA, SM	538	23196	Poso and Mantysaari (1996b)
(0.02)	(0.03)	(0.03)						
0.16	0.13			Holstein	LA, AM	876	224869	Weller and Ezra (1996)
0.16	0.15	0.15		Holstein	LA, SM	1093	596905	Boichard and Rupp (1997)
0.10				Holstein	LA, AM		4247	Detilleux *et al.* (1997)
0.15			0.14	Ayrshire	LA, SM	637	23854	Luttinen and Juga (1997)
0.23			0.19	Holstein		232	10720	
0.14	0.10	0.15		RD	LA, SM			Nielsen *et al.* (1997a)
(0.01)	(0.01)	(0.02)						
0.14	0.15	0.13		DF				
(0.01)	(0.01)	(0.01)						
0.12	0.10	0.15		DJ				
(0.01)	(0.01)	(0.02)						
0.13				Ayrshire	LA, AM		6310	Poso *et al.* (1997)
0.08				Ayrshire	TD, AM			
0.08	0.13	0.14		Holstein	TD, AM		4046096	Reents and Dopp (1997)

[1] Breed: BS, Brown Swiss; RD, Red Danish; DF, Danish Friesian; DJ, Danish Jersey

[2] Model: LA, lactation average, TD test day, SM, sire model; AM, animal model; DM: Non-additive sire and dam model

SCC is usually measured on a scale of cells per millilitre. However its distribution is skewed and variances among herds or groups are heterogeneous. As most statistical methods assume a normal distribution and homogeneity of variance, SCC is commonly transformed to a log scale for analysis. Heritability estimates for log transformed somatic cell counts are shown in Table 1.7, which is based on heritability estimates from studies in the comprehensive review of Mrode and Swanson (1996), but includes some estimates subsequent to that review (Poso and Mantysaari, 1996b; Weller and Ezra, 1996; Boichard and Rupp, 1997; Detilleux *et al.,* 1997; Nielsen *et al.,* 1997b; Poso *et al.,* 1997a and Reents and Dopp, 1997).

The simple average of the heritability estimates presented in Table 1.7 and in the review of Mrode and Swanson (1996) is 0.13. However, there is a large range of estimates (0.03 to 0.39). Recent estimates, since 1995, are between 0.08 and 0.18. Most early studies estimating the heritability of SCC are based on data pre-corrected for fixed effects. Other differences between estimates can be attributed to the type of model fitted (e.g. fixed effects fitted, sire or animal as a random effect) and the estimation procedure.

SCC is measured monthly at the time of milk recording. Thus, in most studies of SCC lactation means of these records were analysed rather than using information from each test day. Lactation averages are usually calculated as arithmetic, geometric, harmonic or the mean weighted by milk yield (Mrode and Swanson, 1996). Wiggans and Shook (1987) argued that the simple arithmetic mean does not account for the effect of stage of lactation at the time of sampling. However, if SCC is measured monthly the effect of stage of lactation would not be significant. In fact, Da *et al.* (1992) showed that the distribution and heritability of lactation SCC computed either as an arithmetic or as a weighted average of test-day SCC were very similar. Based on the results from these and several other studies, Mrode and Swanson (1996) suggested that the simple arithmetic mean of log-transformed test-day SCC is adequate as a lactational measure of SCC.

Test-day models may be more suitable for analysing SCC. Several important short-term environmental effects influence SCC and these are not accounted for by lactation average models, examples include calibration of measuring equipment, age of sample, milking practices (Reents and Dopp, 1997). A particular advantage of the test-day model would be if there was genetic variation between sires for individual lactation curves for SCC, as selection against sires with high SCC early in lactation may be beneficial. One of the main limitations with implementing test-day models is that they are computationally demanding, since each animal has many repeated records, but, as computer technology advances this is becoming less of a problem. Reents and Dopp (1997) analysed a very large data set consisting of over 60 million test-day records for SCC. However, results from Poso *et al.* (1997), showed that no great improvement in accuracy is expected when a test-day model is used rather than a lactation model. They estimated heritabilities were 0.08 and 0.13 for test day and lactation average models.

Table 1.8 Genetic correlation estimates between mastitis and somatic cell counts, s.e.s are shown in brackets

Genetic correlation in lactation				[1]Breed	Source
1	2	3	all		
0.30				Holstein	Weller *et al.* (1992)
0.97				Holstein	Lund *et al* .(1994)
0.37	0.61	0.68		Ayrshire	Poso and Mantysaari (1996b)
(0.12)	(0.10)	(0.12)			
0.65	0.43	0.71		RD	Nielsen *et al.* (1997)
(0.06)	(0.10)	(0.10)			
0.57	0.54	0.54		DF	
(0.04)	(0.04)	(0.06)			
0.00	0.40	0.47		DJ	
(0.14)	(0.12)	(0.14)			

Details of models, numbers of animals etc. where available, are given in Tables 1.6 and 1.7.
[1]Breed: RD, Red Danish; DF, Danish Friesian; DJ, Danish Jersey.

Genetic correlations between SCC and mastitis ranged between 0.30 and 0.97, with most around 0.6 (Table 1.8), suggesting that genes predisposing cows to low cell count also result in a lower rate of infection. There has been controversy over whether selection for low SCC will result in poor resistance to disease, as somatic cells are white blood cells that help combat infection. However, Philipsson *et al.* (1995) found a positive linear relationship between sire breeding values for mastitis

and SCC which, they argued would result in reduced incidences of mastitis rather than a reduced ability to counter infection.

1.3.4 The relationship between production and mastitis

All genetic correlations between mastitis and production traits were positive in this review (Table 1.9), indicating that selection for high milk production has led to an increase in the incidence of mastitis. Phenotypic correlations were generally close to zero.

Table 1.9 Genetic (r_g) and phenotypic (r_p) correlation estimates between mastitis and production, s.e.s are shown in brackets

[1]Lact	[2]Breed	305 day milk		305 day fat		305 day protein		Source
		r_g	r_p	r_g	r_p	r_g	r_p	
all	Hol	0.18	-0.04	0.00	-0.04			Lyons *et al.* (1991)
1	Hol	0.51						Simianer *et al.* (1991)
1	Hol	0.16						Groen *et al.* (1994)
1	Hol	0.37		0.39		0.20		Uribe *et al.* (1995)
1	Ayr	0.46 (0.09)	0.00					Poso and Mantysaari (1996b)
2	Ayr	0.35 (0.10)	0.01					
3	Ayr	0.61 (0.11)	0.02					
1	Ayr	0.53 (0.09)	0.00					Luttinen and Juga (1997)
all		0.49 (0.08)	0.00					
1	Hol	0.31 (0.18)	-0.02					
all		0.31 (0.21)	-0.01					
1	RD					0.24 (0.07)	-0.05	Nielsen *et al.* (1997a)
1	DF					0.34 (0.05)	-0.02	
1	DJ					0.55 (0.11)	-0.05	

[1] Lact: Lactation number
[2]Breed: Hol, Holstein, Ayr, Ayrshire; RD, Red Danish; DF, Danish Friesian; DJ, Danish Jersey.

1.4 Metabolic disorders

1.4.1 Ketosis (Acetonaemia)

Ketosis is primarily a disease of high yielding dairy cows occurring in the first few weeks after calving. Clinical signs include lack of appetite, decreased milk yield, loss of body condition and sweet smelling breath (arising from ketone bodies). In a study of Finnish Ayrshires, Detilleux *et al.* (1994) observed that ketotic cows have a

depressed milk yield in early lactation, equivalent to a loss of 44 kg for 17 days over the diagnosis period. However, milk production over the entire lactation was higher for ketotic than non-ketotic cows. Other factors found to affect the incidence of ketosis include lactation number (the incidence of ketosis is higher in older cows), occurrence in the previous lactation, calving condition score and protein percentage in the previous lactation (Rasmussen *et al.*, 1997).

Table 1.10 Heritability estimates for ketosis in Holstein Friesians

Incidence	[1]Heritability in lactation			[2]Country	[3]Model	Sires	Records	Source
(%)	1	2	all			(n)	(n)	
2.6	0.009			Sweden	LM, SM	190	38164	[4]Eriksson and Wretler (1991)
4.3			0.08	USA	LM, SM	229	9187	Lyons *et al.* (1991)
5	0.09	0.07		Finland	LM, SM	339	28277	Mantysaari *et al.* (1991)
6.8	0.01			Norway	TM, SM	704	208693	Simianer *et al.* (1991)
4.1			0.09	Canada	TM, SM	92	1985	Uribe *et al.* (1995)

[1]Lactation: Heritability estimates in lactations 1, 2 and all
[2]Country: Country of origin of data
[3] Model: LM, linear model, TM, threshold model; SM, sire model
[4] Study of Swedish Friesian Breed, heritability estimate for Swedish Red and White was 0.008

Heritability estimates for ketosis (Table 1.10) are all very low (<10%). In ten studies reviewed by Emanuelson (1988) heritability estimates for ketosis ranged between 5% and 10% (after adjusting for the frequency of ketosis). Mantysaari *et al.* (1991a) found a repeatability between lactations of 0.17, which they suggested may be high enough to warrant inclusion in decisions for culling.

As one of the main symptoms of ketosis is a depression in appetite, a negative energy balance and consequent antagonistic relationship with production may be expected. Mantysaari *et al.* (1991a) estimated that genetic correlations between first lactation ketosis and milk production in first and second lactations were both around 0.17. Second lactation ketosis seemed unrelated to milk production in either lactation. Uribe *et al.* (1995) estimated a genetic correlation of 0.77 between ketosis in all lactations and milk yield using a data set comprising of Holsteins with an overall incidence of 4.1%. Simianer *et al.* (1991) obtained moderate negative genetic correlations between ketosis and fat and protein percentages and suggested that breeding for high butterfat and protein percentages would lead to a reduced incidence of ketosis.

1.4.2 Milk fever (Hypocalcaemia)

Milk fever is associated with a fall of blood calcium levels, which is a consequence of insufficient uptake of calcium around the time of calving. The incidence of milk fever is virtually non-existent in primiparous cattle, but increases gradually from second lactation onwards. As most genetic studies of dairy diseases consider only first lactation animals, there are relatively few genetic parameter estimates for milk fever. If disease recording is on the basis of treatment rather than clinical occurrence, then there may be an over-recording of milk fever, as some herds treat cows with a calcium solution around the time of calving as a preventative measure, regardless of whether cows show signs of milk fever. If cows of high genetic merit only are treated, then there will be problems associated with preferential treatment. A more common strategy to control the incidence of milk fever is to feed a low calcium diet in early lactation as this improves calcium mobilisation in the peri-parturient period. The incidence of milk fever in 90 herds studied Kossaibati and Esslemont (1995) ranged between 0.7% and 22% (mean 7.7%), indicating the importance of herd management factors.

However, milk fever also appears to have a genetic component. Lin *et al.* (1989) reported heritability estimates of 0.30 in second calf cows and 0.42 in older cows. These moderately sized estimates were supported by a study by Lyons *et al.* (1991), who estimated heritabilities of 0.40 (pooled across lactations). Uribe *et al.* (1995) obtained a much lower heritability estimate for milk fever (0.09) using data from 4693 second and greater lactation animals recorded in commercial herds in Ontario. In their study, milk fever had a moderate negative correlation with milk yield, implying that cows of high genetic merit for milk production might be more resistant to this disease. However, they failed to mention whether preventative treatments were administered to high genetic merit cows. If so the correlation estimate will be biased. Preferential treatment of cows in this way would appear to make milk fever a difficult trait to deal with in genetic analyses.

To conclude, it appears that improving the feeding and management of dairy cows may be the most effective strategy in controlling milk fever. But, it is still important to estimate genetic parameters for this trait. If the genetic correlation between milk fever and milk yield is large and unfavourable, then it should perhaps be considered as a future breeding objective.

1.5 Lameness

Lameness is a clinical sign or symptom of a disorder that causes a disturbance in locomotion, and is considered to be the third major disease complex, after mastitis and infertility (Politiek *et al.*, 1986; Boelling and Pollott, 1997). In cattle there are many different types of lameness caused by a variety of disorders and factors. A recent study of the prevalence of lameness in the UK by Murray *et al.* (1996), showed that the most predominant forms were sole ulcers and white line lesions. Together these accounted for 50% of 8645 recorded cases of lameness. The average incidence of lameness in the UK has recently been estimated to be 24 cases per 100 cows (Kossaibati and Esslemont, 1995).

Collick *et al.* (1989) reported that average calving to first service and calving to conception intervals were four and fourteen days longer for lame cows than non-lame cows respectively. Taking reduced fertility and other losses related to lost and discarded milk, veterinary treatments, staff time and a higher risk of culling, Kossaibati and Esslemont (1997) estimated that the average cost of lameness in the UK per affected cow lactation was £274. This estimate was calculated assuming that a lame cow has, on average 1.4 cases per year. Excluding costs associated with culling, longer calving intervals and extra services roughly halves the estimated cost of lameness.

Several non-genetic factors affecting lameness have been identified including herd, age of cow, stage of lactation, season of calving (Politiek *et al.*, 1996). The herd effect is often considered to be the most important. Weaver (1986) estimated that the incidence of lameness in North America and Europe ranged between 3% and 60% on

individual farms. Several factors may be responsible for these differences including: the size of herd, type of housing system, type of diet and amount of hoof-care (e.g. whether hooves are trimmed by a professional hoof trimmer). Although the effect of herd seems to account for much of the variation in lameness, there is some evidence that there is a genetic component.

There are relatively few heritability estimates for lameness. In a recent and comprehensive review by Boelling and Pollott (1997) estimates from five studies were reported. In their review, ten different types of hoof disorders were considered rather than a general lameness category. Most heritability estimates ranged between 0.10 and 0.20. Few studies have considered 'lameness' as a broad category, i.e. lame or not lame in a lactation; estimates for those that have are included in Table 1.11.

Table 1.11 Heritability estimates for lameness in Holstein cattle

[1]Herit	Incidence (%)	[2]Lact	Country	[3]Model	Sires	Records (n)	Source
0.005	1.2	1	Sweden	LM, SM	190	38164	Eriksson and Wretler (1991)
0.16	5.1	all	USA	LM, SM	229	9187	[4]Lyons *et al.* (1991)
0.02	9.3	1	Holland	LM, SM	224	3617	Groen *et al.* (1994)
0.04	9.3	1	Holland	TM, SM	224	3617	Groen *et al.* (1994)
0.016	2.9	1	UK	LM, SM	10845	437	[5]Boelling (1996)

[1]Herit: heritability estimates
[2]Lact: lactation number
[3]Model: LM, linear model, TM, threshold model; SM, sire model
[4]Locomotive disorders
[5]A score for lameness was formed by recoding a 1-5 locomotion score to a binary lameness score

Lyons *et al.* (1991) considered locomotive disorders rather than lameness *per se* and obtained the highest heritability estimate of 0.16. Other estimates range between 0.005 and 0.04. The incidence of lameness was particularly low in the Swedish study of Eriksson and Wretler (1991). The Swedish recording scheme only includes veterinary treated cases and so this figure does not include lameness treated by foot trimmers and farmers. The low incidence is therefore likely to be because only the most severe cases are included in the data.

Estimates of genetic correlations between production and lameness are mostly unfavourable ranging between about 0.2 and 0.4 (Boelling and Pollott, 1996). Uribe *et al.* (1995) investigated culling for leg problems and found more problems in cows of high genetic merit for production as genetic correlations with milk, butterfat and protein yield were positive and moderate (0.27, 0.20 and 0.21 respectively). Corresponding phenotypic correlations were negative (-0.18, -0.19 and -0.23). Implying that cows of high genetic merit are more susceptible to lameness than those of low genetic merit, but lameness seems to cause a suppression of milk yield and hence negative phenotypic correlations.

1.6 Linear type scores as predictors of health and fertility traits

Type classification systems evolved to provide a description of the physical attributes of cows, especially those related to health, longevity or show-ring success. Many early schemes were subjective, classifying cows according to some sort of desired optimum. Most dairying countries now use linear assessments which were originally developed in the USA in the late 1970s and early 1980s. In the UK the conformation of dairy cattle is assessed using a linear scoring system in which animals are evaluated for sixteen type traits, the minimum and maximum values of which are the biological extremes of each trait. This scheme is operated by the Holstein Friesian Society of Great Britain and Ireland (HFS), details of which are given by Holstein Friesian Society (1995) and Brotherstone (1994). These records are used to provide a physical description of cows and to enable predictions of breeding values for both cows and bulls. A description of the traits recorded by the HFS and recent heritability estimates are given in Table 1.12.

Although in the past a lack of uniformity of type traits recorded in classification schemes has hindered the use of type information from other countries, there has been much effort in recent years to standardise methods of linear type classification used internationally. The availability of converted type proofs will ensure that type traits can be used as an international selection tool where appropriate.

Table 1.12 Descriptions and heritabilities of linear type traits recorded by the Holstein Friesian Society of Great Britain and Ireland (Dr S Brotherstone, personal communication; in Simm, 1997)

Type trait	Minimum	Maximum	Heritability
Stature	Small	Tall	0.48
Chest width	Narrow	Wide	0.27
Body depth	Shallow	Deep	0.35
Angularity	Coarse	Angular	0.26
Rump angle	High pins	Low pins	0.29
Rump width	Narrow pins	Wide pins	0.22
Rear leg set, side view	Posty	Sickled	0.19
Foot angle	Low	Steep	0.27
Fore udder attachment	Loose	Tight	0.27
Central ligament[1]	Broken	Strong	0.16
Udder depth	Below hocks	Above	0.39
Rear udder height	Low	High	0.20
Teat placement rear	Wide	Close	0.43
Teat placement side	Close	Apart	0.41
Teat length	Short	Long	0.44

[1] Formerly called Udder support

1.6.1 The relationship between type and lameness

There are particular problems with recording and using actual incidences of lameness in breed improvement programmes. Clinical cases of lameness are not easy to identify accurately. The incidence of lameness in the four different studies shown in Table 1.11 varied immensely. While this may be a reflection of environmental factors e.g. housing, diet and the types of organisms that are most prevalent etc., it may also reflect differences in recording proficiency. Recording lameness accurately would require training veterinarians and farmers to record consistently and on a daily basis. This is why, for lameness in particular, using linear type traits or hoof characteristics scored once or twice on large numbers of young cows may be more effective for selection purposes. However, clinical cases of lameness still need to be recorded in some herds to establish this relationship accurately.

Boelling (1997) encouraged the use of hoof characteristics and locomotion to improve resistance to lameness. Based on the findings of his review, McDaniel (1995) recommended that selection for high foot angles, straighter legs from the side

and rear, and improved locomotion can reduce the incidence of lameness within herds.

1.6.2 The relationship between type and mastitis

In most studies the relationship between linear type traits and somatic cell counts has been considered rather than the relationship with clinical mastitis. The simple reason for this is that more countries collect and evaluate SCC records, the rationale being that the correlation between SCC and mastitis is considered to be large enough that reductions in SCC would also lead to a decreased incidence of mastitis. Consequently, studies of the relationship between SCC and type are mainly from countries where genetic evaluations for SCC, but not mastitis, are available. In this review all studies of this relationship were from North America. In some studies type and SCC records measured on cows have been considered (e.g. Seykora and McDaniel, 1986; Monardes *et al.,* 1990; Rogers *et al.,* 1991; Reents *et al.,* 1995a), while others have investigated the relationship between predicted transmitting abilities of bulls (PTAs) for SCC and type (e.g. Schutz *et al.,* 1993; Rogers *et al.,* 1995).

Very few genetic associations between body and feet and leg characteristics are significantly different from zero, although there are exceptions. For example, significant genetic relationships with SCC have been found for thurl width (Rogers *et al.,* 1991; Schutz *et al.,* 1993) and dairy form (Schutz *et al.,* 1993; Rogers *et al.,* 1995). Some udder conformation traits seem to be reasonable predictors of SCC. Teat length is one such trait. Significant genetic correlations with SCC have been found and range between 0.20 and 0.40. Thus longer teats are associated with higher SCC (Seykora and McDaniel, 1986; Rogers *et al.,* 1991; Rogers *et al.,* 1995). Teat length was also found to be related to longevity (e.g. Brotherstone and Hill, 1991). Deeper udders were related to higher SCC (e.g. Rogers *et al.,* 1991; Reents *et al.,* 1995a; Schutz *et al.,* 1993). In the literature reviewed, there seems to be a general consensus that a combination of several type traits should be used to reduce SCC. For example, Schutz *et al.* (1993) found in their study that four of the best five traits

to predict SCC were non-udder traits: thurl width, strength, dairy form and body depth. This is somewhat surprising, as udder characteristics usually have the strongest correlations with mastitis. For example, using selection index theory, Rogers (1993) suggested that selection for lower somatic cell scores, higher udders and closer teat placement would be the most effective traits to help to reduce or eliminate undesirable correlated responses in mastitis associated with selection for high milk production.

Lund *et al.* (1994) used Danish data to investigate relationships between clinical mastitis, somatic cell count and udder conformation. The largest genetic correlation was between teat length and clinical mastitis, (-0.72; longer teats are associated with an increased probability of mastitis, as shorter teats receive higher scores in the Danish linear type scoring scheme). Contrary to some of the North American findings, no relationship was found between teat length and SCC. In addition, Lund *et al.* (1994) found similar moderate genetic correlations between dairy character and both SCC and mastitis (0.37 and 0.32), indicating that more angular cows are more prone to mastitis. However, their analysis did not include an adjustment for milk yield, and so this correlation with dairy character is partly an indirect expression of the relationship between milk yield and mastitis. Groen *et al.* (1994) found that udder conformation was positively related to mastitis, which was surprising, which seems to indicate that better udder conformation would result in a higher incidence of clinical mastitis. They gave several reasons for this apparent anomaly: i) the threshold model used did not converge after 30 rounds of iteration; ii) several proven bulls with a large impact on the data set had high PTAs for udder type, but poor PTAs for mastitis resistance; iii) a linear relationship between type and mastitis was assumed, but the relationship between type and SCC may have been non-linear.

1.6.3 The relationship between type and fertility

Few studies have investigated the relationship between fertility and linear type scores. Dadati *et al.* (1986) found moderate genetic correlations between calving

interval and several type traits including chest floor (-0.42), rear udder (-0.37), capacity (-0.34) and dairyness (-0.43). This implied that stronger, less dairy cows with shallow udders had shorter calving intervals. However, the model they fitted did not adjust for production, and some correlations may therefore be overestimated.

Chapter 2

Genetic parameters for health and fertility using data from Scottish Livestock Services

2.1 Introduction

There are various reasons why breeding programmes should consider health and fertility traits. Of these, the most important is that single trait selection for milk and its components has led to a decline in levels of health and fertility. Most disease and fertility traits have low heritabilities, but genetic variances of some are considered to be large enough to include in selection programmes (Chapter 1). However, with the exception of Scandinavia, few countries consider health and fertility as breeding objectives in their breeding programmes. Inclusion of health and fertility traits, in most countries, has been limited by a lack of reliable data.

Several dairy recording services in the UK now offer comprehensive recording of health, fertility and culling information. The data used in this study were obtained from Scottish Livestock Services Ltd (SLS). SLS started recording health disorders in 1994. In order to encourage as many farmers to record health disorders as possible, there is no charge for this service. Although not all members participate, enough information on health, fertility, production, pedigree and culling among other things has accumulated to use the data for a genetic analysis of health and fertility traits.

The aims of this study were to i) estimate genetic parameters for some common health disorders and several measures of fertility in cows of all lactations in data from one of these schemes, and in a subset of this data set comprising only heifers ii) estimate correlations between health, fertility and milk yield.

2.2 Material and methods

2.2.1 Data

Data on production, health and inseminations recorded by SLS were available for cows with completed lactations (i.e. at least two calving dates) between January 1994 and February 1996. Health and service details were recorded on farms and collected on a monthly basis to correspond with official milk recording visits by SLS. Health records consisted of the date of the disease incidence and an identifying code (chosen from 7 different codes - see Table 2.1). Service records included dates of inseminations. Milk yields were available for all animals.

Animals had unique identification themselves; all of the animals had sire identification and many also had dam identification. In addition, as many grand-parent herdbook numbers as possible were traced. Only animals sired by North American or European Holstein bulls were retained.

Herds were initially selected according to the completeness of their records. For example cows with fertility information were kept from herd-years where at least 60% of the cows with milk yield records had one or more insemination dates. This apparently low criterion was set to allow for animals being culled. Herds with adequate health records could not be selected in the same way, because imposing a minimum criterion may mean that herds with a genuinely low incidence of disease may be excluded. As the risk of selecting herds with poorly recorded health incidences would also be high, herds with 0% health disorders and herds where the only health reason recorded was 'other' in each herd-year were dropped from the analyses.

Two data sets were constructed: (i) data for all lactations and (ii) data for heifers only, by matching health and service information from the selected herds to pedigree and milk production data. Thus, each animal had to have a milk production record and either a health or a fertility record or both.

As a successful insemination was determined by a subsequent calving date, animals included in the fertility data had to have complete lactations. This structure allowed a range of traits to be calculated including: (i) calving interval (CI), the interval between consecutive calving dates; (ii) days to first service (DFS), the interval between calving and first insemination date; (iii) the interval between calving and conception date (CON); (iv) services per conception (SPC), the number of inseminations in a lactation; (v) conception to first service (FSC), coded as 1 or 0 for success or failure respectively.

In order to eliminate abnormally long lactations, days to first service of less than 20 days and greater than 200 days were deleted, as were calving intervals of greater than 700 days. Records were also deleted for calving intervals less than 300 days as these were likely to be abortions. Gestation length was restricted to between 262 and 302 days (20 days either side of the mean value for gestation length). Records with abnormal gestation length were not deleted, instead CON, FSC and SPC were set as missing.

The data editing procedure reduced the health data set to 58% of the original number of records and the fertility data to 52% of the original number of records. In the health data set, many herds simply did not record health disorders, or recorded health disorders poorly. Most fertility records were lost because many of the cows did not have two consecutive calving dates. The numbers of records in the final data sets are shown in Table 2.2.

The frequency of a cow getting more than one occurrence of a particular health disorder was generally low, hence health disorders were recoded in binary form, i.e. 0 for no observations of a particular disease and 1 for one or more observation of a disease in a given lactation. Only records where the lactation length was greater than 200 days were accepted. Many animals with health information, but no fertility information, had complete lactations and therefore 2 consecutive calving dates

recorded. Consequently the calving interval for these records could also be calculated, providing extra information for this trait.

Table 2.1 Health disorders recorded by members of the SLS

Disease code	Disorder
1	Breeding Problems
2	†Milk fever (hypocalcaemia)
3	†Mastitis
4	†Foot problems
5	Staggers (hypomagnesia)
6	Ketosis (acetonaemia)
7	Other

Analyses were restricted to the categories marked †, as the other categories were either ambiguously defined (other and breeding problems) or the incidence was very low (staggers and ketosis).

Table 2.2 Number of records in the data sets after editing

	All lactations	Heifers only
Number of records	33732†	9163
Animals	27444	9163
Sires	2224	913
Herd-year-seasons	2458	1701
Herds	410	401

† 30%, 24%, 17%, 11% and 18% of records were for 1st, 2nd, 3rd, 4th, and 5th+ lactation groups respectively.

2.2.2 Statistical methods

Observations were assigned to herd-year-season subclasses using four seasons at calving (January to March, April to June, July to September, and October to December). Cows in lactation five or above were grouped into the same lactation class. Preliminary analyses were done to determine which fixed effects and covariates should be fitted in the statistical models. Herd-year-season, lactation number and age as a quadratic and linear term were all found to significantly affect the traits analysed ($P<0.05$). Calving month and days in milk were fitted to models in preliminary analyses, but found to be unimportant and therefore not included in the final model. The percentage of North American Holstein genes was not fitted, as many animals were not pedigree registered and therefore did not have this information. It would have been desirable to include the service sire also, as conception is a function of both male and female fertility, however, this information was not available. The final model was chosen on the basis of the results from the preliminary analysis. The model used for national genetic evaluations of milk production traits in the UK (Animal Data Centre, 1996) includes the following

environmental pre-adjustments: age within lactation, lactation number, month of calving, calving interval, heterogeneity of variance, percentage heterosis and percentage recombination. In the analysis presented here, fitting calving interval to milk yield may have led to problems in estimating covariances with fertility traits, as all the fertility traits are clearly closely related to calving interval.

The statistical model used to estimate variance components for heritabilities, permanent environmental effects and correlations described below was fitted to each trait:

$$Y_{ijkl} = \mu + a_i + c_i + HYS_j + L_k + b_1A + b_2A^2 + e_{ijkl}$$

where Y_{ijkl} = record with effects as follows:

μ = overall mean

a_i = random effect of cow i

c_i = random permanent environmental effect of cow i

HYS_j = fixed effect of herd-year-season j

L_k = fixed effect of lactation k

$b_1A + b_2A^2$ = linear (b_1) and quadratic (b_2) regression coefficients on age in months (A)

e_{ijkl} = random error term

Age at calving was fitted as a linear and quadratic covariate. Lactation number was fitted separately as a fixed effect. A permanent environmental effect was included in the first data set (all lactations) to account for multiple lactation records for the 6288 cows with repeated records. The same model was fitted to the second data set (heifers) except that the terms for permanent environmental effects and lactation number were dropped.

The Variance Components and Estimation (VCE) restricted maximum likelihood (REML) programme written by Groeneveld (1996) was used to analyse the data.

Both data sets were initially analysed using univariate and then bivariate animal models. The intention was then to analyse both data sets with multivariate models, fitting all health and fertility traits plus milk yield. However, while this was feasible for the smaller data set (heifers only), computational limitations meant that a multivariate model could not be used for the entire data set (all lactations). Heritabilities and permanent environmental effects for the multiple lactations data set were estimated using univariate models and correlations between traits were estimated using bivariate models. All parameter estimates for the heifer data set were using the multivariate model.

Gianola and Foulley (1983) suggested that threshold models (TMs) are theoretically well suited for the analysis of discrete data. However, because of restrictions associated with the level of recording detail available from field data, the use of threshold models in this case may be inappropriate. There are two main limitations with the threshold model approach: i) the data have to be filtered in order to have at least one incident per sub-class and ii) the approximate nature of the analysis based on Taylor series expansions. Many herd-year-season subclasses had no disease occurrences, which was a direct consequence of the low overall incidence of disease in these data. Despite these constraints, a subset of the mastitis data was constructed according to these requirements and analysed using a univariate threshold model without a relationship matrix in the Generalised Linear Mixed Models (GLMM) programme in GENSTAT (Lawes Agricultural Trust, 1993). The data subset used in the GLMM analysis was approximately one third of the size of that used in the VCE analysis. The heritability estimate obtained using GLMM cycled between 0.04 and 0.07 in the latter stages of iteration (with large associated standard errors; 0.04). This can be interpreted as a failure of the iterative process to distinguish between two apparent local maxima and hence converge, even after a considerable period of computer processing time. There may have been several contributory reasons for this, including the small size of data set and the approximate nature of the analysis, making it difficult for the procedure to match the precision of the VCE analysis. Because of these problems, GLMM was not used to estimate heritabilities for the

other 0/1 traits. Variance components for all subsequent analyses were therefore estimated using VCE.

In bivariate VCE analyses of both data sets, calving interval and interval between calving and conception were found to have a genetic correlation close to one, as were number of services per conception and conception to first service. Calving interval is the interval between calving and conception plus the gestation length which was restricted to be between 262 days and 302 days. Therefore, it is not surprising that these two traits are closely correlated. Conception to first service is simply the number of services per conception recoded as a 0/1 trait. The heritabilities of calving interval and conception to first service were higher than those for calving to conception and number of services per conception. So multivariate and bivariate analyses of the data sets excluded calving to conception and number of services per conception.

2.3 Results

Means corrected for fixed effects of fertility traits were similar for heifers and cows in all lactations (Tables 2.3 and 2.4). Heifers had a 4 day longer calving interval and took 2 days longer to first service than cows. The incidence of mastitis and lameness was higher in cows of all lactations than heifers. Milk fever seldom occurs in heifers, so it was only analysed in the multiple lactations data set.

Table 2.3 Number of records (n), means and phenotypic standard deviations (σ_p) of the traits in all lactations, after fitting fixed effects. Heritabilities (h^2) and permanent environmental effects (c^2) and their respective s.e.s

Trait	Abbreviation	n	Mean	σ_p	h^2	s.e.(h^2)	c^2	s.e.(c^2)
305 day milk yield (kg)	MILK	33732	6455	1078	0.34	0.01	0.19	0.01
Calving interval (days)	CI	29049	387	45	0.032	0.005	0.000	0.000
Calving to conception (days)	CON	21725	101	40	0.028	0.007	0.005	0.028
Days to 1st service (days)	DFS	24155	84	25	0.031	0.007	0.000	0.000
No. of services per conception	SPC	21725	1.5	0.84	0.003	0.007	0.005	0.004
Conceived to 1st service	FSC	21725	0.66	0.46	0.019	0.009	0.000	0.000
Milk fever	MFEV	15280	0.026	0.15	0.080	0.009	0.000	0.000
Mastitis	MAST	15280	0.088	0.26	0.071	0.012	0.002	0.001
Lameness	LAME	15280	0.049	0.20	0.026	0.008	0.013	0.013

Means and standard deviations are after fitting fixed effects.

Table 2.4 Number of records (n), means and phenotypic standard deviations (σ_p) of the traits in heifers. Heritabilities (h^2) and their respective s.e.s

Trait	abbreviation	n	mean	σ_p	h^2	s.e.(h^2)
305 day milk yield (kg)	MILK	9163	5765	898	0.49	0.04
Calving interval (days)	CI	9163	391	48	0.053	0.012
Calving to conception (days)	CON	6718	106	48	0.027†	0.013
Days to 1st service (days)	DFS	7506	86	26	0.041	0.015
No. of services per conception	SPC	6718	1.5	0.94	0.019†	0.004
Conceived to 1st service	FSC	6718	0.66	0.49	0.026	0.010
Mastitis	MAST	3486	0.046	0.20	0.053	0.016
Lameness	LAME	3486	0.038	0.14	0.073	0.025

Means and standard deviations are after fitting fixed effects.
† Analyses were with univariate models, all other estimates were from the multivariate analysis.

Heritability estimates for milk yield were moderate to high, and higher for heifers than cows of all lactations. Conversely, heritability estimates for fertility and health traits were low, ranging from 0.003 for SPC to 0.080 for milk fever in cows of all lactations and from 0.019 for SPC to 0.073 for lameness in heifers. Permanent environmental effects for health and fertility traits ranged from 0.000 to 0.015. Consequently, repeatabilities of these traits were low.

Table 2.5 Genetic (below the diagonal, with s.e.s) and phenotypic (above the diagonal) correlations between health and fertility traits and 305 day milk yield in all lactations

Trait	MILK	CI	DFS	FSC	MAST	MFEV	LAME
MILK	-	0.22	0.16	-0.13	0.01	0.05	0.02
CI	0.50 (0.06)	-	0.51	-0.62	0.03	0.03	0.02
DFS	0.43 (0.08)	0.93 (0.08)	-	0.08	0.00	0.02	0.02
FSC	-0.19 (0.11)	-0.56 (0.11)	0.15 (0.20)	-	-0.02	-0.01	-0.02
MAST	0.21 (0.06)	0.06 (0.13)	-0.18 (0.15)	-0.19 (0.17)	-	0.06	0.02
MFEV	0.19 (0.06)	0.03 (0.10)	0.25 (0.13)	0.03 (0.05)	0.64 (0.11)	-	0.02
LAME	0.29 (0.11)	0.07 (0.14)	0.18 (0.19)	0.70 (0.21)	0.17 (0.17)	0.21 (0.21)	-

Table 2.6 Genetic (below the diagonal, with s.e.s) and phenotypic (above the diagonal) correlations between health and fertility traits and milk yield in heifers

Trait	MILK	CI	DFS	FSC	MAST	LAME
MILK	-	0.20	0.17	-0.03	0.004	0.02
CI	0.32 (0.07)	-	0.50	-0.63	0.04	0.02
DFS	0.48 (0.09)	0.90 (0.06)	-	0.04	0.04	0.02
FSC	0.05 (0.10)	-0.79 (0.08)	-0.52 (0.12)	-	-0.02	-0.01
MAST	-0.40 (0.09)	-0.47 (0.15)	-0.29 (0.23)	0.15 (0.23)	-	0.007
LAME	0.24 (0.06)	0.24 (0.14)	-0.32 (0.17)	-0.30 (0.21)	-0.41 (0.23)	-

For most traits genetic correlations were larger than phenotypic correlations (Tables 2.5 and 2.6). Genetic correlations between milk yield and calving interval, days to first service and lameness were positive in both data sets. The negative correlation between MILK and FSC in the entire data set (all lactations) indicates that cows with higher genetic merit for milk yields were less likely to conceive to the first insemination.

The genetic correlation between mastitis and milk yield differs markedly between the two data sets: 0.21 and -0.40 for multiple lactations and heifer data respectively. Heifers of high genetic merit for milk yield appear to be less prone to mastitis, whereas the reverse appears to be the case for older cattle.

In both data sets the genetic correlation between calving interval and days to first service was close to one. Conception to first service (FSC) was negatively correlated with calving interval. FSC was a 0/1 trait: where zero was failure to conceive to the first service and one was conception to the first service. Consequently negative correlations with FSC are unfavourable.

2.4 Discussion

Many records were lost from the data set during the editing procedure, but this was expected as the recording system is relatively new, and it is applied in commercial herds and most farmers using it attach higher priority to recording production of milk

and its components. Some producers record insemination information (service dates and sires) which is required to register pedigree calves and also for management purposes, e.g. to calculate drying off dates. More service data were available than health data, which is probably a reflection of perceived value of the two types of information. Although health information may be useful to identify animals to cull, most farmers know which cows have persistent health or fertility problems without the need for written records. However, rather than relying on memory to determine which animals should be culled there is an obvious benefit in having written records, as more objective and reasoned culling reasons can be determined. Clearly, as health and fertility issues are becoming more important, there is a need to encourage more farmers to collect this type of data both from a farm management perspective and for sire evaluations.

The incidences of health disorders were lower in this study than in a recent survey of dairy health and fertility from herds, mostly in the south of England, participating in the Dairy Information Service recording system (DAISY; Kossaibati and Esslemont, 1995). The incidence of mastitis was 9% for cattle of all lactations in this study and 21% for cows of all ages in the DAISY herds (Kossaibati and Esslemont, 1995). Means for conception to first service and number of services per conception in this study were lower than in the DAISY herds, although means for calving interval, calving to conception interval and days to first service were slightly higher in this study. This suggests that, although cows were inseminated fewer times on average, intervals between calvings were no better in this study than those found in the DAISY herds, due perhaps to under-recording of service information. The data editing procedure used here biased the fertility records towards those animals that conceived to first inseminations, as records were restricted to animals with gestation lengths between 262 and 302 days and cows had to have two consecutive calving dates to be included in the fertility data. Moreover, cows that were culled for failure to conceive, or those that were culled in the first 200 days of lactation for poor health or low milk yield were excluded from the data. Therefore, cows with the poorest health, production and fertility were excluded. This could potentially have influenced

our results, and in particular correlations with milk yield. Hoekstra *et al.* (1994) and Ouweltjes *et al.* (1996a) used similar data editing procedures to analyse fertility data in Dutch cattle, only including complete lactations; the means in both these studies were very similar to those reported here. The data editing procedure used in our study restricted fertility data to records with two consecutive calving dates. This is currently the only way to determine conception in the UK. If reliable pregnancy diagnosis information were available, incomplete lactations could be retained and non-return rates calculated rather than FSC this would mean that more records would be available for analysis and would reduce the potential problem of bias.

The heritability estimate of milk yield agrees well with that reported by Brotherstone (1994) of 0.47 for pedigree first lactation cattle. Visscher and Thompson (1992) estimated the heritability of milk yield as 0.39, 0.29, 0.23 for cows in first, second and third lactations respectively. The repeatability of milk yield in this study was 0.53 ($h^2 + c^2$), which is close to the repeatability estimate of 0.56 between first and second lactations obtained by Visscher and Thompson (1992). Estimated heritabilities for both health disorders and fertility were low which is consistent with literature estimates. Emanuelson (1988) suggested that differences between farmers in recording adequacy could lead to reduced heritability estimates and a large unexplained residual variance.

In this study, mastitis had the largest heritability of all diseases analysed (0.053 to 0.071), which is similar to the estimate obtained by Eriksson and Wretler (1991) of 0.020 for cows of all ages. Uribe *et al.* (1995) found a heritability of zero for cows in all lactations and a heritability of 0.15 for cows in their first parity. However, comparisons of heritability estimates of binary traits should be made on the assumed underlying scale, rather than the 0/1 scale, as they are affected by the incidence or proportion affected. The conversion formula $p(1-p)/z^2$ (Robertson and Lerner, 1949) can be used to transform heritabilities from the 0/1 to underlying scale, where p is the population incidence and z is the height of the ordinate of a standardised normal at

the threshold point corresponding to p. Heritability estimates for mastitis on the underlying scale were 0.23 and 0.25 for heifers and all lactations respectively.

Mantysaari *et al.* (1991b) used a data simulation approach to investigate the issue of bias in genetic parameter estimates of two 0/1 traits at three different incidences (0.25, 0.15 and 0.05). They looked at a half-sib design with a number of fixed effects, but no genetic relationships between sires. The heritabilities of both traits were 0.2 and the genetic correlation between the traits was 0.5. It was reported that the heritability estimates, after transformation to the underlying scale, did not significantly differ from the true values. However, other research suggests that the the Robertson and Lerner formula tends to overestimate the heritability on the underlying scale when the incidence is extreme (McGuirk, 1989).

As far as genetic correlations are concerned, threshold theory predicts that the genetic correlation estimated on the binomial scale should be a direct estimate of that on the liability scale, i.e. it does not need to be transformed. This is because the genetic variances and correlations on the liability scale are similarly affected by transformation to the threshold scale. Phenotypic correlations between 0/1 traits are expected to be biased downwards, as they are influenced by the incidence. Mantysaari *et al.* (1991b) observed that residual correlations estimated with a linear model were 49, 52 and 58% of the true value at the incidence levels 0.05, 0.15 and 0.25, respectively. They concluded that the threshold model does have a major advantage over linear methods for estimating residual correlation (and hence phenotypic correlation), but for estimating heritabilities and genetic correlations the threshold model does not show a significant improvement over linear methods.

Although the heritability of mastitis is very low, it is a common and economically important disease (Kossaibati and Esslemont, 1995) and therefore a likely candidate for inclusion in future breeding programmes. An alternative would be to increase the resistance to clinical mastitis by using a trait correlated to clinical mastitis. For

example, selection for low somatic cell count has been proposed (Philipsson *et al.*, 1995) and is being practised in several countries.

Heritability estimates for fertility traits ranged from 0.003 to 0.053, which are in good agreement with literature estimates (see Chapter 1).

The genetic correlation between milk yield and mastitis in this study was 0.21 for the multiple lactations data set, and agrees well with estimates of Lyons *et al.* (1991) who obtained a genetic correlation of 0.18 pooled across lactations. Lower producing cattle that have mastitis are more likely to be culled than higher producing cattle which have mastitis. This may bias the phenotypic correlation between mastitis and milk yield upwards, and perhaps bias the genetic correlation by a small amount. The estimate of the genetic correlation between mastitis and milk yield in heifers was negative in sign (-0.41), whereas most previous estimates of genetic correlations between mastitis and milk yield in heifers are moderate and positive, e.g. Uribe *et al.* (1995) estimated a correlation of 0.37 and Simianer *et al.* (1991) obtained an even higher estimate of 0.51. However, there were only 3486 mastitis records for heifers in this study compared to 15280 mastitis records for heifers and cows. Hence the results presented for heifers need to be treated with caution.

The positive correlations between milk yield and fertility traits (Tables 2.5 and 2.6) indicate that selection for high milk yield leads to a deterioration in fertility. However, these correlations may be misleading. If high milk producing cows are given more opportunities to rebreed, or if breeding is delayed in high production cows, the association between production and fertility will be biased by management decisions (Philipsson, 1981; Bagnato and Oltenacu, 1994). Parameter estimates for days to first service, calving interval and number of services per conception are those most likely to biased in this respect. However, determining a suitable way to measure the fertility status of a cow is important, if fertility is to be included in a breeding programme. Some authors have advocated the use of non-return to first service, as it is less affected by farmer decisions for individual cows (e.g. Boichard and Manfredi,

1994; Hoekstra *et al.*, 1994). The equivalent trait in this study was conception to first service (FSC). The heritabilities for FSC were 0.019 for cows of all lactations and 0.026 for heifers.

The incidence of production diseases in first lactation animals is low, but generally increases with parity (Emanuelson *et al.*, 1993; Beaudeau *et al.*, 1995). Where the disease causes a reduction in yield and sires are evaluated on multiple lactations from daughters there may be some indirect selection against disease. In progeny testing schemes for binomial traits, predicted breeding values of sires are based mainly on the incidence of the trait in daughter groups; the incidence is known more precisely when daughter groups are large. Therefore, predicted breeding values of sires with large progeny groups are less influenced by the incidence of the trait than when progeny groups are small.

Analysis of 0/1 traits such as disease and conception to first service (FSC) is often done using statistical methods specifically designed to deal with their non-normality, such as threshold models (e.g. Weller and Ron, 1992). Adequate non-linear models for multivariate estimation and prediction of categorical data are still to be developed. An important question is whether the difference between estimated variance components using non-linear versus linear methods is enough to warrant use of non-linear methodology. Analysis using REML techniques has been shown to be satisfactory even when the incidence is close to 0 or 1, providing family sizes are large and the heritability is not very high (see McGuirk 1989, for a review). Weller and Ron (1992) obtained highly correlated solutions of fixed and random effects for linear and threshold models, indicating that using threshold models may merely provide theoretical improvements to the estimation procedure. If genetic parameters estimated using a linear model, such as VCE, are similar to those obtained using programs designed for binomially-distributed data, then the advantages of using VCE, e.g. fitting an animal model with a pedigree, outweigh the disadvantages of using VCE, e.g. the assumption of normality.

Breeding for disease resistance should be considered in future breeding schemes as the moderately sized unfavourable genetic correlations between milk yield and mastitis, milk fever and lameness in the all lactations data set give reason for concern. The amount of genetic variation may be sufficient to breed for improved disease resistance and fertility through progeny testing schemes, if progeny test sires have large enough daughter groups to achieve sufficient accuracy.

Recordings of health disorders and service information should be encouraged. The incidence of health disorders was lower here than in other UK studies. This is more likely to be due to under-recording than to a better level of health. More precise recording would reduce the error variance, heritabilities would increase and selection would be more accurate. As more health and fertility data are collected, more precise estimates of heritabilities and correlations will be obtained.

Chapter 3

Estimation of genetic parameters using data from a health and fertility management recording system

3.1 Introduction

Most heritability estimates for health and fertility, reviewed in Chapter 1, were estimated using field data from national recording schemes. Differences in the type of model fitted, estimation procedure etc., however, make it difficult to draw inferences about the relative merits of the various recording schemes. It is possible that the method of recording data affects parameter estimates. Thus, one of the main aims of this study was to estimate genetic parameters for similar health and fertility traits to those investigated in Chapter 2, but using data from a health and fertility management recording system, the Dairy Information System (DAISY). Strandberg *et al.* (1996) emphasised that research on genetic improvement of traits other than production should focus on definition and recording of traits. Genetic parameter estimates obtained from recording schemes with different objectives may be useful for designing future recording schemes.

DAISY is a comprehensive commercial dairy recording scheme which includes, in some detail, health and fertility. The information is collected and used by DAISY members (either independently or in conjunction with a veterinarian) for management purposes. The scheme was set up in the 1970's and has gradually expanded, but, until now there have been insufficient data to enable estimation of genetic parameters of health and fertility traits.

Most measures of fertility are based on insemination and calving dates and include non-return rates, conception to first service, calving interval, days to first service, days to conception date, etc. However, there is no standard measure of fertility across countries (Banos, 1996; Chapter 1). Health disorders are usually recorded as

categorical data and whether an animal is ill or not is determined subjectively. A reduction in the incidence of mastitis is possible by selection for lower somatic cell counts in milk (e.g. Lund *et al.,* 1994; Schutz, 1994; Philipsson *et al.*, 1995).

The distribution of somatic cell counts is positively skewed. Ali and Shook (1980) suggested that a logarithmic transformation of SCC was the best method of obtaining a normal distribution. Somatic cell score (SCS), is the $\log_2$ transformation of SCC ($SCS = \log_2(SCC/100)+3$). This transformation is used by the National Co-operative Dairy Herd Improvement Program of the USA (Shearer *et al.,* 1992). As an indicator of both clinical and subclinical mastitis, SCC has several desirable attributes: the heritability of SCC is higher than that of clinical mastitis; SCC has a continuous distribution, and the correlation between SCC and mastitis is reasonably high (Emanuelson, 1988).

There is evidence to suggest that linear type traits are important predictors of longevity (e.g. Brotherstone and Hill, 1991), mastitis (e.g. Lund *et al.,* 1994), somatic cell count (e.g. Rogers *et al.,* 1991; Lund *et al.,* 1994; Rogers *et al.,* 1995) and lameness (e.g. Boelling and Pollott, 1997). Linear type traits are measured on a relatively large scale and international conversions are available for Predicted Transmitting Abilities (PTAs) of many type traits. Some type traits, in particular those related to the udder and leg, are perceived by many breeders, to be important for resistance to mastitis and lameness. In most countries (except Scandinavia) direct recording of health events is not yet practised. Therefore, it seems appropriate to investigate the relationship between type and health traits.

The aims of this study were: i) to estimate genetic parameters for several measures of fertility, health disorders and production using data from the DAISY database; ii) to estimate heritabilities for the same trait in the first three lactations; iii) to investigate whether genetic parameters estimated using data from a recording scheme designed specifically to record health and fertility traits (i.e. DAISY) differ to literature estimates from national recording schemes; and iv) to examine the potential use of

linear type scores as predictors of health traits by regressing the phenotypic measurement for each animal on the sire's predicted transmitting ability for type.

3.2 Material and Methods

Data were available from 33 herds recording information on health, fertility and milk and its components, between 1st January 1988 and 31st December 1994. Data were recorded either on farm by individual farmers or in conjunction with a veterinarian operating the DAISY computerised system as a bureau for clients (Esslemont, 1993).

Each record included a combination of health, fertility and 305 day production data. In all cases lactation length had to be over 200 days in order to be included in the data. Production traits included projected or actual 305 day milk, butterfat and protein yields. Health traits analysed included mastitis, lameness SCS. The majority of mastitis and lameness cases were diagnosed and recorded by the farmer. Two herds did not have any recorded cases of mastitis or lameness and therefore, only records for fertility and production were used from these two herds. Several herds did not have records for SCS.

In order to determine whether an insemination resulted in a successful pregnancy, only records with a subsequent calving date were accepted for the fertility data. Several traits were calculated including: (i) calving interval, the interval between two consecutive calving dates; (ii) days to first service, the interval between calving and first insemination date; (iii) the conception to first service coded as 1 or 0 for success or failure respectively. Fertility records were discarded if days to first service were less than 20 or greater than 200 days, if calving intervals were outwith the range 300 to 700 days and if gestation lengths were over 20 days either side of the mean value of 282 days.

Most herds used in this study were not registered with a breed society, although to be included in the data set, all cows had to be sired by a Holstein bull. Only records for animals with sire identification were retained. Most sires were identified by

abbreviated versions of the sire's full name. Sire names and consequently pedigree herdbook numbers were deciphered from the abbreviations, if in doubt records were discarded. Thus, most animals had their paternal grandparents identified and these were included in the pedigree file. Where dams had pedigree herdbook numbers or their own record, maternal grandparent information were also included in the pedigree file. Only sires with more than 5 daughters were retained.

The editing procedure reduced the data set by 39%: 49% of these records were lost because sires were not identified and 51% were discarded where animals were culled before finishing a lactation, or because records exceeded the minima and maxima criteria for calving interval, days to first service and gestation length.

Cows in lactations five and above were grouped together as one lactation class. Cows were also grouped into herd-year-season subclasses, with four seasons defined according to month of calving (January to March, April to June, July to September and October to December).

The following analyses were carried out:

1) Data set 1 included all lactation records for animals after the editing procedure and consisted of 10569 records for 4642 cows by 224 sires in 430 herd-year-seasons. Genetic parameters were estimated using the variance components and estimation (VCE) restricted maximum likelihood (REML) programme written by Groeneveld (1996). A multivariate animal model with all traits fitted simultaneously was used to estimate (co)variances between traits. The model included (i) herd-year-season, (ii) lactation and (iii) age at calving as a linear and quadratic regression within each lactation. In addition, a permanent environmental effect was fitted as an additional random effect to account for multiple lactation records (some animals having more than 1 lactation record). The health disorders (mastitis and lameness) were initially coded as a 0/1 trait, records were coded as one where a cow had one or more disease incidences within a lactation. The incidence of both mastitis and lameness increased

with lactation number. This may lead to problems in (co)variance component estimation when linear models are used instead of threshold models, as the mean and variance are linked. Variances within each lactation subclass were fixed to one, while means were maintained at their original values by recoding mastitis and lameness according to the probability of 1's (p) and 0's (q) within each lactation. The 0's were recoded to $p - ap$ and 1's recoded to $p + aq$ with $a = \sqrt{1/pq}$.

2) Heritabilities were also estimated for each of the traits in first, second and third lactations separately using VCE REML. The model used was the same as that described previously, but without lactation number and permanent environmental effect terms. Mastitis and lameness were analysed as 0/1 traits.

3) A subset of data set 1 was used to investigate the relationship between sire predicted transmitting abilities (PTAs) for type and health disorders for daughters of these sires (mastitis and lameness). The Holstein Friesian Society of Great Britain and Ireland (HFS) operates a linear type classification scheme, details of which are given by Holstein Friesian Society (1995) and Brotherstone (1994). Most of the data used in this study were from non-pedigree registered herds, so few cows had linear type scores, therefore sire PTAs for type were used in this analysis. There were sixteen type PTAs, in addition to PTAs for temperament and ease of milking. In this study 'type traits' refers to all of these PTAs. Records were retained where the sire had a minimum reliability of 65% and at least five daughters in the data. The data set included 3500, 7024 and 6523 daughter records for SCS, mastitis and lameness respectively. There were 157 sires. Daughter phenotypic measurements for mastitis, lameness and SCS were regressed on sire PTAs for linear type traits fitted one at a time using GENSTAT REML (Lawes Agricultural Trust, 1993). The model fitted included (i) herd-year-season, (ii) lactation number, (iii) age as a linear and quadratic covariate. In addition to this, another model was fitted that included herd-year-season, lactation and age, and also sire PTAs for milk yield. This was to check that

some of the regressions that were significantly different from zero did not arise because of a correlation between the health traits and milk yield.

3.3 Results

Heritabilities and phenotypic standard deviations for 305 day milk, butterfat and protein yields, health and fertility traits obtained from multivariate REML, using data from all lactations (data set 1), are shown in Table 3.1. The heritability estimates for mastitis, lameness and the fertility measures were low, ranging from 0.047 for lameness to 0.013 for conception to first service, the heritability of SCS was 0.15. Heritability estimates for production traits were moderate to high, 0.33, 0.27 and 0.27 for milk, butterfat and protein yields respectively.

Table 3.1 Numbers of records (n), means and phenotypic standard deviations (σ_p), heritabilities (h^2) and permanent environmental (c^2) effects for data set 1

Trait	Abbreviation	n	Mean	σ_p	h^2 (s.e.)	c^2 (s.e.)
305 day milk yield (kg)	MILK	10004	6733	1067	0.33 (0.01)	0.31 (0.01)
Butterfat (kg)	BFAT	4611	260	45	0.27 (0.01)	0.26 (0.01)
Protein (kg)	PROT	4611	209	36	0.27 (0.01)	0.26 (0.01)
Calving interval (days)	CI	10569	382	46	0.017(0.002)	0.026 (0.002)
Days to 1st service (days)	DFS	10569	70	18	0.020 (0.003)	0.029 (0.003)
Conception to 1st service (0/1)	FSC	10569	0.51	0.49	0.013 (0.002)	0.027 (0.003)
Somatic cell score	SCS	5151	3.25	1.07	0.15 (0.01)	0.28 (0.01)
Mastitis	MAST	10512	0.15	1.0	0.045 (0.006)	0.049 (0.004)
Lameness	LAME	9476	0.15	1.0	0.047 (0.005)	0.035 (0.004)

Table 3.2 Genetic (below diagonal) and phenotypic (above diagonal) correlations between health and fertility traits and milk production traits

	MILK	BFAT	PROT	CI	DFS	FSC	SCS	MAST	LAME
MILK	-	0.69	0.71	0.18	0.09	-0.13	-0.08	-0.03	0.03
BFAT	0.92 (0.01)	-	0.73	0.16	0.08	-0.12	-0.10	-0.02	0.01
PROT	0.99 (0.01)	0.96 (0.01)	-	0.16	0.09	-0.12	-0.10	0.02	-0.01
CI	0.28 (0.06)	0.53 (0.05)	0.36 (0.06)	-	0.33	-0.59	0.12	0.04	0.05
DFS	0.41 (0.06)	0.37 (0.06)	0.42 (0.06)	0.56 (0.08)	-	0.04	0.05	0.02	0.03
FSC	-0.12 (0.08)	-0.35 (0.07)	-0.20 (0.08)	-0.81 (0.06)	-0.13 (0.13)	-	-0.08	-0.03	-0.03
SCS	0.16 (0.04)	0.11 (0.05)	0.14 (0.04)	0.28 (0.09)	0.16 (0.09)	-0.40 (0.06)	-	0.23	0.04
MAST	0.29 (0.05)	0.27 (0.05)	0.29 (0.05)	0.16 (0.09)	-0.14 (0.07)	-0.58 (0.07)	0.65 (0.05)	-	0.03
LAME	0.13 (0.06)	0.12 (0.06)	0.13 (0.06)	0.33 (0.09)	-0.11 (0.11)	-0.65 (0.06)	0.26 (0.08)	0.48 (0.10)	-

Standard errors are shown in brackets
Abbreviations are in Table 3.1

Genetic correlations between health and fertility traits and milk yield were in all cases antagonistic (Table 3.2). Correlations with milk yield ranged between 0.13 and 0.41. The genetic correlations between the production traits were greater than 0.90. Correspondingly, correlations between all production traits and the health and fertility traits were very similar. However, the correlations between butterfat yield and calving interval and butterfat yield and conception to first service were approximately double the equivalent correlations with milk yield.

The highest genetic correlations between traits other than production were between conception to first service and calving interval (-0.81) and SCS and mastitis (0.65). More cases of mastitis, lameness and higher SCSs were associated with longer calving intervals and days to first service and lower conception to first service.

Table 3.3 Number of records (n), means, phenotypic standard deviations (σ_p) and heritabilities (h^2) of the traits in the first three lactations

	1st lactation				2nd lactation				3rd lactation			
	n	mean	σ_p	h^2 (s.e)	n	mean	σ_p	h^2 (s.e)	n	mean	σ_p	h^2 (s.e)
MILK	2701	5910	1228	0.47 (0.06)	2168	6813	1521	0.50 (0.06)	1672	6995	1497	0.22 (0.04)
CI	2881	387	52	0.072 (0.03)	2303	379	46	0.016 (0.01)	1774	380	49	0.054 (0.04)
DFS	2881	74	24	0.017 (0.02)	2303	70	21	0.005 (0.01)	1774	69	21	0.029 (0.03)
FSC	2881	0.51	0.50	0.026 (0.04)	2303	0.52	0.50	0.001 (0.01)	1774	0.51	0.50	0.062 (0.04)
SCS	1317	2.7	1.2	0.25 (0.07)	1158	3.0	1.2	0.25 (0.08)	885	3.2	1.2	0.47 (0.10)
MAST	2862	0.09	0.29	0.11 (0.04)	2290	0.11	0.32	0.22 (0.06)	1767	0.14	0.35	0.21 (0.05)
LAME	2603	0.10	0.30	0.038 (0.03)	2057	0.12	0.33	0.095 (0.04)	1576	0.14	0.35	0.015 (0.02)

Abbreviations are in Table 3.1

Table 3.3 shows numbers of records, means, standard deviations and heritabilities of the traits in the first three lactations. As expected, milk yield increased with lactation number. Calving interval and days to first service were longer in first lactation animals than second or third lactation animals. SCS, mastitis and lameness increased with parity. The incidence of mastitis and lameness in fourth and fifth and greater lactation groups were even higher, so the overall incidence of mastitis and lameness in data set 1 was 0.15 (Table 3.1).

The heritability of conception to first service was much higher in first and third lactation animals (0.026 and 0.062) than for second lactation animals (0.001). Heritability estimates for calving interval and days to first service were also lowest in second lactation animals. Heritability estimates for mastitis in the first three lactations were higher than the estimate obtained from analysing all lactations, ranging between 0.11 and 0.22. Within lactation heritability estimates ranged from 0.015 to 0.095 for lameness and from 0.25 to 0.47 for SCS.

Table 3.4 Regression coefficients (b) (x 100) of the health traits on sire PTAs for type

			SCS		Mastitis		Lameness	
Type trait	Min.	Max.	b	s.e.	b	s.e.	b	s.e.
Total merit	Negative	Positive	1.10	2.60	1.26*	0.54	0.47	0.58
Stature	Small	Tall	2.10	2.20	1.17**	0.45	0.75	0.48
Chest width	Narrow	Wide	-3.37*	2.27	1.31**	0.49	1.57**	0.53
Body depth	Shallow	Deep	0.003	2.20	1.63***	0.46	0.96*	0.49
Angularity	Coarse	Angular	3.21*	2.30	0.53	0.48	-0.13	0.49
Rump angle	High	Low pins	-6.38***	2.09	-1.19**	0.43	-1.16**	0.44
Rump width	Narrow	Wide	-3.56*	1.87	0.75*	0.36	0.57	0.38
Rear leg set	Posty	Sickled	-2.35	2.25	-0.38	0.47	-0.26	0.49
Foot angle	Low	Steep	-5.24*	2.31	-0.47	0.47	-0.11	0.49
Fore udder attachment	Loose	Tight	0.47	2.74	1.32*	0.55	1.13*	0.56
Udder support	Broken	Strong	5.08**	2.59	2.06***	0.52	-0.20	0.55
Udder depth	Below	Above	2.33	2.62	0.28	0.52	0.60	0.53
Rear udder height	Low	High	-4.89**	2.22	-1.69***	0.48	0.60	0.51
Teat placement rear	Wide	Close	1.64	2.73	-1.16*	0.61	-0.40	0.63
Teat placement side	Close	Apart	-3.55	2.03	0.48	0.43	0.19	0.44
Teat length	Short	Long	1.34	2.57	0.77	0.56	0.79	0.59
Temperament	Nervous	Quiet	-5.71***	1.73	-0.16	0.35	0.22	0.38
Milking ease	Slow	Fast	0.87	1.01	0.41	0.24	0.18	0.24

Table 3.5 Regression coefficients (b) (x 100) of the health traits on sire PTAs for type after adjustment for sire PTA for milk yield

			SCS		Mastitis		Lameness	
Type trait	Min.	Max.	b	s.e.	b	s.e.	b	s.e.
Total merit	Negative	Positive	2.98	2.88	1.34*	0.60	0.84	0.63
Stature	Small	Tall	3.43	2.35	1.20**	0.49	1.01*	0.50
Chest width	Narrow	Wide	-3.28*	2.27	1.30**	0.49	1.57**	0.53
Body depth	Shallow	Deep	0.98	2.34	1.70***	0.49	1.22**	0.51
Angularity	Coarse	Angular	5.81***	2.61	0.46	0.53	0.14	0.55
Rump angle	High	Low pins	-6.69***	2.10	-1.17**	0.42	-1.19**	0.44
Rump width	Narrow	Wide	-3.22**	1.92	0.72	0.37	0.69	0.39
Rear leg set	Posty	Sickled	-2.60	2.26	-0.34	0.48	-0.32	0.49
Foot angle	Low	Steep	-5.73**	2.33	-0.43	0.48	-0.20	0.49
Fore udder attachment	Loose	Tight	0.21	2.75	1.33**	0.55	1.11*	0.56
Udder support	Broken	Strong	9.27***	3.05	2.62***	0.62	0.17	0.66
Udder depth	Below	Above	1.76	2.68	0.34	0.52	0.52	0.54
Rear udder height	Low	High	6.74**	2.39	1.69***	0.52	0.90	0.55
Teat placement rear	Wide	Close	1.65	2.74	-1.17*	0.61	-0.43	0.63
Teat placement side	Close	Apart	-3.56*	2.03	-0.47	0.43	0.18	0.44
Teat length	Short	Long	1.66	2.58	0.74	0.56	0.90	0.60
Temperament	Nervous	Quiet	-5.60***	1.74	-0.16	0.35	0.20	0.38
Milking ease	Slow	Fast	0.83	1.02	0.41	0.24	0.20	0.24

Regressions of mastitis, lameness and SCS on type traits are shown in Tables 3.4 and 3.5. The model fitted to obtain the estimates in Table 3.5 included sire PTA for milk yield fitted as a covariate. This was because some of the regressions that were significantly different from zero, in Table 3.4, may have arisen due the positive genetic correlations between milk production and the health traits. Three of the regressions significant at the $P<0.05$ level in Table 3.5 were not significant in Table

3.4. The regressions of health traits on linear type scores presented in this study are based on relatively few records and should be considered as preliminary. Furthermore, as significance tests are applied to large numbers of regressions (and therefore some regressions would be expected to be significant by chance), the results should be treated with caution, particularly where regressions significantly differ from zero at the $P<0.05$ level.

Regressions of mastitis and SCS on half of the type traits were significantly different from zero ($P<0.05$). Of these, four and three of the significant regressions for mastitis and SCS respectively were related to the udder. Regressions on udder support were highly significant ($P<0.001$) for mastitis and SCS; stronger udder support was associated with an increased probability of mastitis and a higher SCS. Regressions on chest width were significant for all three health traits, with a wider chest width being associated with more cases of mastitis and lameness, but lower SCS. When the fertility traits were regressed on sire PTAs for type, the only significant regressions were on chest width, a narrow chest width being associated with longer calving intervals and lower conception to first service.

3.4 Discussion

Records were lost for several reasons: i) the animal's sire could not be identified; ii) the sire was not Holstein Friesian; iii) the animal did not have two consecutive calving dates, usually as the animal was culled before calving again. Therefore, the selection of data was in some ways biased towards the healthiest, most fertile cows, as the poorest (in terms of health and fertility) were culled before calving again.

Calving interval and days to first service were longer in first lactation animals than older animals. Poor fertility is the predominant culling reason in first and second lactation animals (Kossaibati and Esslemont, 1995). Calving intervals and days to first service may be longer in heifers than cows because some farms may calve heifers earlier in the season, lengthening the interval between calving to first service.

Linear models are commonly used to analyse binomially distributed data in preference to threshold models, because the advantages of using linear models are expected to outweigh the disadvantages. Advantages of linear models are that they allow a higher computing speed and often allow fuller relationship matrices to be fitted than threshold models. The main disadvantage is the assumption of normality. An additional assumption is that variances within fixed effect subclasses are constant. However, the incidence of both mastitis and lameness increased with increasing lactation number. As the mean and variance are linked in binomial distributions, this may lead to estimation problems. The method described here adjusted within lactation variances to one, while maintaining the same overall mean. However, although this method has theoretical advantages, parameter estimates were smaller than heritability estimates obtained when the variance within lactation was not adjusted. Using the same data and model, heritabilities for mastitis and lameness analysed as 0/1 traits were 0.075 and 0.055 respectively.

In the study reported in Chapter 2 (analysis of SLS data), the mean for conception to first service was higher than here, but mean calving intervals were very similar in the two data sets. The recorded incidences of mastitis and lameness in Chapter 2 were 0.09 and 0.05 respectively. The incidences of both mastitis and lameness in the present study were 0.15. This may imply under-recording in some SLS herds (Chapter 2). One of the aims of the present study was to examine whether genetic parameters estimated using data collected from a scheme designed specifically for recording health and fertility differed from parameter estimates from a national scheme. This information may be useful in defining which traits to improve through selection programmes, and in aiding the design of future recording schemes. Detailed recording schemes might be expected to give more reliable and higher parameter estimates than field recording schemes where under-recording may be a problem. Higher heritabilities would be expected as a consequence of less unexplained or error variance.

In Chapter 2 heritability estimates obtained for mastitis and lameness were 0.071 and 0.025 using SLS data. As the incidence of mastitis and lameness differed between the two studies, it may be more informative to compare heritabilities after transformation from the observed to the underlying scale, using the conversion formula of Robertson and Lerner (1949):

$$\frac{p(1-p)}{z^2}$$

where p is the population incidence and z is the height of the ordinate of a standardised normal at the threshold point corresponding to p. Heritabilities on the underlying score for mastitis (scored as 0/1) were 0.226 and 0.176 for SLS and DAISY data sets respectively and for lameness (scored as 0/1) were 0.114 and 0.129 for SLS and DAISY data sets respectively. Observed and underlying heritabilities for mastitis and lameness were similar for the two data sets and were larger on the underlying scale than the observed scale in both cases. For all traits, the heritability estimates obtained in Chapter 2 were very similar to the heritability estimates here. This indicates that, in this instance, the parameter estimates obtained were little affected by the recording scheme.

The heritability of SCS in this study was 0.15 (Table 3.1). Mrode *et al.* (1995) found a heritability estimate of 0.11 for SCS using data from the first three lactations in UK Holstein Friesian cattle. Within lactation, the heritabilities for SCS ranged from 0.25 to 0.45 (Table 3.2). There were relatively few records for SCS, which may have led to convergence problems in estimating within lactation variance components. In a larger study, Poso and Mantysaari (1996b) obtained heritability estimates of 0.15, 0.16 and 0.14 for first, second and third lactation Finnish cattle.

Correlations were also estimated between traits in lactations one, two and three. This should have provided information on whether health and fertility traits could be treated as the same trait across lactations. However, associated standard errors were high and so correlations are not presented here. This could have been because the data sets were relatively small and perhaps also because genetic links were weak. The

means for conception to first service were very similar in lactations one to three (0.51 to 0.52). The highest heritability for conception to first service was for first lactation animals (0.026), which is the same as the estimate obtained in Chapter 2. When transformed to the underlying scale, heritability estimates for conception to first service were 0.043 and 0.041 for SLS (Chapter 2) and DAISY heifers respectively. The heritability of conception to first service in second lactation cattle was much lower, which could be responsible for the low overall heritability of this trait.

SCS has been used as a selection criterion for mastitis (Philipsson *et al.,* 1995). There was a moderately high correlation between mastitis and SCS of 0.65 and the heritability of SCS was substantially higher than mastitis (0.15 and 0.045 for SCS and mastitis respectively). Thus, selection to reduce the incidence of mastitis via indirect selection using SCS may be possible.

The genetic correlations between milk yield and health and fertility traits were antagonistic (Table 3.2). This indicates that selection for high milk yield leads to a deterioration in health and fertility. Many previous studies have found antagonistic correlations between milk production and health traits (e.g. Lyons *et al.,* 1991; Uribe *et al.,* 1995) and between milk yield and fertility traits (e.g. Van Arendonk *et al.,* 1989; Oltenacu *et al.,* 1991; Hoekstra *et al.,* 1994; Poso and Mantysaari, 1996a).

Lameness and mastitis were positively correlated with days to first service and calving interval and negatively correlated with conception to first service, implying that cows with poorer fertility also had poorer health. Peeler *et al.* (1994) found that if a cow became lame in the period before service there was less chance of observing oestrus. A cow with one or more cases of lameness in a lactation is not as reproductively fit as a healthy cow.

Several regressions of health traits on sire PTAs for type were significantly different from zero, indicating that some type traits may potentially be useful as selection criteria when the breeding goal includes health. Although many farmers see obvious

benefits from recording health and fertility traits, as they can use the information for management purposes, national recording schemes for health (except for SCS) and fertility do not yet exist, or are relatively new, except in Scandinavian countries. Easily measured traits, such as type traits, may be useful in the interim, or may augment health and fertility recording. SCS would seem to be an obvious selection criterion for mastitis. However, the accuracy of selection may be increased by incorporating several type traits. The regressions of health traits on linear type scores presented in this study are based on relatively few records and should be considered as preliminary. As more data becomes available, a fuller investigation of the relationship between health traits and type will be possible.

Due to the unfavourable correlations between milk production and health and fertility traits, future breeding programmes should include measures or indicators of health and fertility traits. The heritabilities and genetic variances estimated in this study seem to indicate that selection to improve some or all of these traits will be possible, although slow. The correlation between mastitis and SCS and the relatively high heritability of SCS suggest that further reductions in mastitis incidence may be achieved through indirect selection using SCS. The method of choice for improvement of health and fertility traits would be to include some of them in future versions of the UK index for total economic merit (ITEM; Veerkamp *et al.*, 1995a) with a weighting based on their economic values. However, there may be justification for increasing the weighting given to health traits further, because of animal welfare implications and associated public opinion.

Chapter 4

Genotype and feeding system effects and interactions for health and fertility traits

4.1 Introduction

There is considerable value in studying populations of cows selected solely on milk production traits, and to assess the consequences of this strategy on traits other than production. The literature includes several such studies in the USA and Europe (e.g. Bonczek *et al.*, 1992; Dunklee *et al.*, 1994; Jones *et al.*, 1994; Simm *et al.*, 1994 and McGowan *et al.*, 1996). Both Simm *et al.* (1994) and McGowan *et al.* (1996) reported studies on the same high producing dairy herd as reported in the present study.

The introduction of milk quotas in the European Union in 1984 has led to greater interest in low input systems as a way to keep the costs of production down. However, there are concerns that energy intake (input) is unlikely to match milk production (or output) in early lactation, which may lead to an increase in body tissue mobilisation (Veerkamp and Emmans, 1995). This may be a particular problem when diets high in forage are fed to high genetic merit dairy cattle. A possible consequence of such differences between input and output could be increased health and fertility problems. For this reason it is important to investigate genotype by environment interactions (G x E) for health and fertility traits.

A long-term experiment was established at the University of Edinburgh / Scottish Agricultural College Langhill Dairy Cattle Research Centre in 1973. The herd is split into two genetic groups: a selection line (S) and control line (C). The main objective is to study consequences of long-term selection for fat plus protein yield on a number of traits. In 1988, two different diets were introduced to investigate whether the

advantages of high genetic merit dairy cattle are maintained on lower input systems for a wide range of production and non-production traits.

The aims of the present study were: (i) to investigate the effects of genotype on a range of health traits and measures of fertility; (ii) to investigate the effects of two feeding systems on health and fertility; (iii) to test for a possible interaction between genotype and feeding system on health and fertility traits and (iv) to estimate genetic parameters for health and fertility traits.

4.2 Material and methods

Records were obtained from the Langhill Dairy Cattle Research Centre. The data used here covered a period from September 1980 to August 1996. All cows were Holstein Friesian. The calving period for animals in this study was from September to January. Cows were housed in conventional cubicle housing from calving until July.

4.2.1 Genetic lines

The animals at Langhill are divided into two genetic groups: a selection (S) and control (C) line. The S line cows are bred to bulls with the highest Predicted Transmitting Abilities (PTAs) for fat plus protein yield available in the UK. Sires of the C line animals are of about UK average genetic merit for kg fat plus kg protein yield. The S and C lines were established to investigate the effect of selection on production, food intake, health, fertility and profitability. Each year, four to five bulls per line are selected and, except for matings between close relatives, are mated randomly within the lines. Bulls known to give a high incidence of calving difficulties are not used on heifers. The herd replacement rate is around 25%. Heifers are calved at two years and are selected mainly on the basis of their pedigree index (0.50 x sire's PTA for fat plus protein plus 0.25 x maternal grandsire's PTA for fat plus protein) but with some regard to expected date of calving.

4.2.2 Diets

During the housed period, complete diets based on grass silage and concentrates were fed *ad libitum* through Calan Broadbent gates, allowing individual feed intakes to be recorded. Until 1988 all animals were fed a relatively high concentrate diet of about 2.5t concentrates per year. Since 1988 two feeding regimes have been used, a high concentrate diet (HC) and a low concentrate diet (LC) with S and C animals represented in each feeding system. The feeding regimes were designed to achieve the following proportions (in total dry matter) of concentrates, brewers' grains and silage of 20 : 5 : 75 (LC) and 45 : 5 : 50 (HC). The animals on the HC diet had an annual average concentrate intake of about 2.5t and the LC animals had an average annual intake of about 1.0t. Higher proportions of concentrates were fed in early lactation, so that problems arising from underfeeding in early lactation were avoided. Thus dry matter silage content was increased on completion of 100 days and 200 days of lactation. Details of the feeding regime are given by Veerkamp *et al.* (1995b).

4.2.3 Records

All reproduction events were recorded, and included the first observed oestrous cycle, dates and number of services, pregnancy difficulties and calving difficulties. Cows that had not been seen in oestrus by 56 days *post-partum* were routinely checked by the veterinarian for reproductive problems and treated if necessary. Fertility measures were calculated using calving dates (where available) and insemination dates and included: conception to first service (FSC); days to first heat (DFH); calving interval (CI); days open (DOP) and days to first service (DFS). In addition to these measures, a fertility disorder category was also recorded and included cows shown to the veterinarian for oestrus not observed (ONO) within 56 days after calving by the farm staff.

All health events were recorded using a three digit numerical code which indicated the general category for the disease as well as the specific disease problem. Health events were recorded by the veterinarian or by farm staff onto recording sheets. This information was then transferred to a computer database. Health records included

mastitis, ketosis, metritis, retained placenta, milk fever and lameness. Some of these health categories resulted from disorders being grouped together, for example all types of lameness (e.g. interdigital dermatitis, sole ulcer etc.) were grouped together into one category. All health disorders were recoded in binary form, i.e. 0 for no observations of disease and 1 for one or more cases of a disease in a lactation; the health trait categories, apart from mastitis and lameness, rarely occur more than once in a lactation. Lameness and mastitis were coded in two ways: as 0/1 traits and according to the actual number of recorded cases in a lactation. Routine hoof trimming commenced in 1985.

4.2.4 Analysis

The data were analysed using Restricted Maximum Likelihood (REML) and Generalised Linear Mixed Models (GLMM) in the GENSTAT computer program (Lawes Agricultural Trust, 1993). Wald statistics, which approximate a χ^2 distribution, were used to test for significance of the fixed effects in a series of univariate analyses. For each analysis the fixed effect of interest was fitted last to the model. GENSTAT REML and GLMM were also used to estimate means for each fixed effect after adjustment for the other fixed effects, with cow fitted as a random effect to account for the covariance between lactations of cows with more than one lactation. GLMM was used to analyse the 0/1 traits, i.e. the health disorders, ONO and FSC. REML was used to analyse all other traits. Estimated means from REML for 0/1 traits were very similar to the GLMM estimates. The advantage in using GLMM rather than REML is that no constant variance is assumed across fixed effect classes.

Two data sets were used in the GENSTAT analyses. The first data set was used principally to investigate the effects of feeding system and genetic line and possible interactions between these effects on the health and fertility traits. The data were selected for the period from September 1988 to August 1996 and comprised 1243 records. In addition to genetic line and feeding system, year and month of calving and lactation number were also fitted as fixed effects. Preliminary analyses had

shown that age at calving and Holstein percentage were not significant after fitting lactation number. Therefore neither of these effects were used in the final model. As fertility is affected by both the male and female, it would be advantageous to include the effect of male fertility in the analysis. However, on this farm insemination sires are chosen at random within lines. Therefore, if a cow is inseminated more than once her fertility is affected by more than one sire and it becomes difficult to use all of this information. The exception to this is FSC, where the effect of the service sire of the first insemination may be investigated. However, the sire at first insemination did not significantly affect FSC and was therefore not included in the final model. Hence, the statistical model used to investigate the effects of genetic line and feeding system was:

$$Y_{ijklmno} = \mu + a_i + c_i + Y_j + M_k + Y_j * M_k + L_l + G_m + F_n + G_m * F_n + e_{ijklmno}$$

$Yijklmno$	= record with effects as follows:
μ	= overall mean
a_i	= random effect of cow
c_i	= permanent environmental effect
Y_j	= fixed effect of year of calving
M_k	= fixed effect of month of calving
L_l	= fixed effect of lactation number (1, 2, 3, 4 and 5+)
G_m	= fixed effect of line (Selection S and Control C)
F_n	= fixed effect of diet (High Concentrate HC; High Forage HF)
$e_{ijklmno}$	= random error term

The second analysis was to investigate more closely the effects of genotype by substituting genetic line with pedigree index (0.50 x sire's PTA for fat plus protein plus 0.25 x maternal grandsire's PTA for fat plus protein). Pedigree index (PI) is a more accurate indicator of genetic merit than genetic line, as there was some overlap in PI between selection and control lines. The contribution of Langhill records to

PTAs was small, as PTAs are estimated using national data. Thus regression coefficients of phenotypic values on PI are equivalent to genetic regressions (Veerkamp *et al.,* 1995b). Therefore, regression coefficients reflect the changes in health and fertility traits as a consequence of selecting bulls for fat plus protein yield. The first data set, described above, was combined with earlier data from the same feeding system. This data set covered the years September 1980 to August 1996, and included records on 2506 lactations. The model used for this analysis included terms for the year and month of calving and the interaction between these two effects, lactation number and feeding system. Animal was fitted as a random effect. The covariate PI was fitted last to the model and regression coefficients were estimated using a series of univariate models.

The second data set (1980-1996), was also used to estimate variances of the traits using the Variance Components and Estimation REML program (VCE; Groeneveld, 1996). VCE was used in preference to GENSTAT as a relationship matrix including all relatives can be fitted. Most animals had sire, dam and grandparent information. The incidence of 0/1 traits and correspondingly the variance may differ between lactations, which may cause problems in estimating (co)variance components. Consequently, variances within lactation were adjusted to one, while means were maintained at their original value by recoding the data according to the probability of 1's (p) and 0's (q) within each lactation. The 0's were recoded to $p - ap$ and 1's recoded to $p + aq$ with $a = \sqrt{1/pq}$ (Chapter 3).

The model fitted to all the traits included: year, month, year by month interaction, lactation number and feeding system. Heritabilities were estimated for all traits using univariate animal models with a permanent environmental effect fitted.

4.3 Results

Table 4.1 Wald statistics obtained from GLMM (for 0/1 traits) and REML (for all other traits), each term tested was fitted last in the model

	Y	M	Y x M	L	G	F	G x F
df	7	4	28	4	1	1	1
Mastitis	13.1	8.5	23.3	50.0***	0.3	0.1	0.3
Ketosis	9.8	12.0*	15.6	30.9***	0.4	0.3	0.1
Metritis	64.1***	1.3	47.0*	9.3	3.4*	0.5	1.4
Retained Placenta	4.8	4.2	8.9	11.8*	1.4	0.0	0.0
Milk fever	3.8	3.8	37.5	85.1***	2.1	8.0**	0.2
Lameness	56.6***	4.7	23.3	26.4***	2.5	0.8	1.7
ONO	61.7***	10.0*	14.9	3.1	10.1***	0.1	0.4
FSC	5.4	5.7	34.9	11.5*	4.0*	0.2	1.0
DFH	41.3***	27.2***	39.0	5.5	25.7***	8.4**	0.0
CI	22.0**	8.5	45.4*	3.2	7.2**	0.1	3.2
DOP	29.6***	12.3*	37.8	3.0	14.4***	0.7	0.4
DFS	23.8***	61.6***	37.2	6.6	12.9***	8.3**	0.9

ONO: Oestrus not observed
FSC: Conception to first service
DFH: Days to first heat
CI: Calving interval
DOP: Days open
DFS: Days to first service

Table 4.1 shows Wald statistics and associated levels of significance for each of the fixed effects in the model. The effect of the year of calving was significantly different from zero ($P<0.01$) for metritis and lameness and all the measures of fertility except for FSC. The month of calving was highly significant for both DFH and DFS ($P<0.001$). DFS is longest, while DFH is shortest in September. DFH is the number of days from calving to first observed oestrus, so cows calving earlier in the calving season appear to resume oestrus sooner than later calving cows. DFS is affected by management decisions. As this farm's policy is to start each calving season in September, early calving cows have a longer period before insemination resumes. A line by year interaction was investigated for all traits and was found to be significant at the $P<0.05$ level for both DFH and DFS, with the difference in DFH and DFS between S and C lines increasing with year of calving. Figure 4.1 shows DFH for S and C lines from 1988/1989 to 1995/1996.

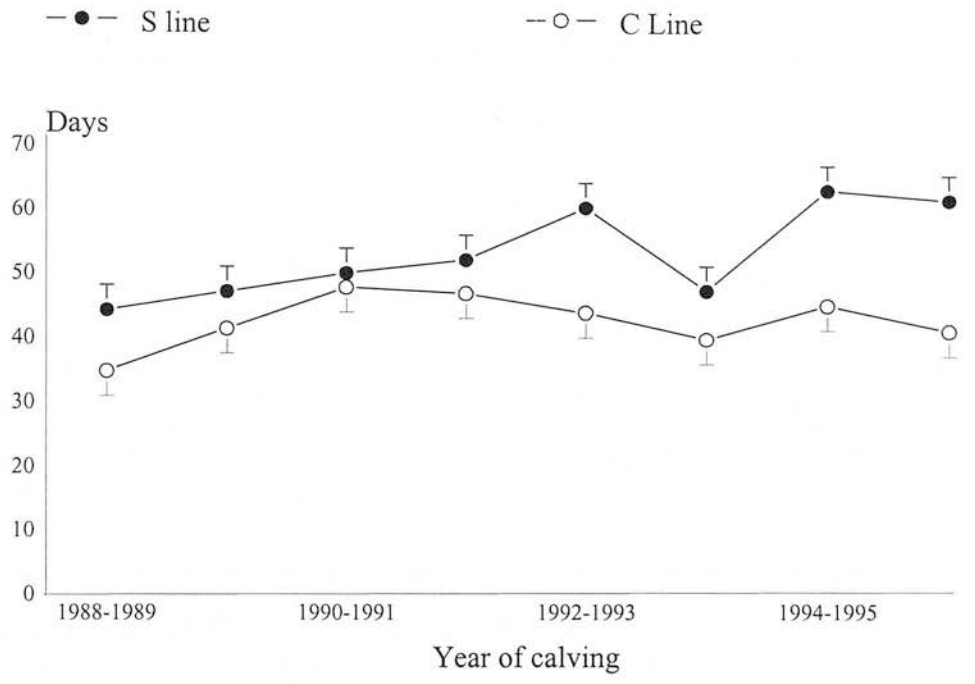

Figure 4.1 Days to first heat (DFH) in the selection (S) and control (C) line

The effect of lactation number was significantly different from zero for all of the health disorders (except metritis), but was not significant for any of the fertility measures except for FSC (Table 4.1). Predicted means for traits in the lactation groups, where the effect of lactation number was significant ($P<0.05$), are shown in Table 4.2. The probability of one or more cases of disease in a lactation increased significantly with increasing lactation number. Significant differences between genetic lines were found for metritis, ONO, FSC, DFH, CI, DOP and DFS (Table 4.1). Predicted means for genetic line and feeding system, for all traits, are shown in Table 4.3. ONO was higher in the selection line than the control line, (0.16 and 0.11 respectively; $P<0.001$). DFH, CI, DOP and DFS were all significantly longer in the selection line cows, the difference between S and C cows exceeding 10 days for DFH, CI, and DOP. Feeding system was significant for milk fever, DFH and DFS (Table 4.3). There were more cases of milk fever and both DFH and DFS were longer for cows fed the HC diet. There were no significant genetic line by feeding

system interactions, so all observed line differences applied to both of the dietary treatments. However, the interaction approached significance (P<0.1) for CI.

Table 4.2 Predicted means of the health disorders and FSC in lactations 1 to 5+ estimated in GENSTAT GLMM after adjustment for fixed effects and random effect of cow

Lactation	1	2	3	4	5+
Number of records	417	284	204	138	200
Mastitis	0.053 (0.009)	0.072 (0.012)	0.126 (0.017)	0.250 (0.028)	0.179 (0.021)
Ketosis	0.007 (0.002)	0.062 (0.007)	0.068 (0.009)	0.125 (0.013)	0.084 (0.010)
Retained Placenta	0.037 (0.009)	0.030 (0.011)	0.049 (0.015)	0.097 (0.026)	0.081 (0.019)
Milk fever	0.000 (0.000)	0.004 (0.003)	0.105 (0.014)	0.295 (0.025)	0.398 (0.022)
Lameness	0.068 (0.009)	0.112 (0.012)	0.135 (0.016)	0.174 (0.021)	0.188 (0.017)
FSC	0.39 (0.03)	0.43 (0.03)	0.46 (0.04)	0.51 (0.05)	0.35 (0.04)

Significance levels for lactation number are all P<0.05, and are given in Table 4.1.
Standard errors are in brackets and are approximate, as the model was non linear

Table 4.3 Predicted means (standard errors) for genetic line and feeding system after adjusting for the fixed effects and cow as a random effect

	Line (G)			Feeding system (F)		
Trait	S	C	P<	LC	HC	P<
Mastitis	0.12 (0.01)	0.11 (0.01)	n.s.	0.11 (0.01)	0.11 (0.09)	n.s.
Ketosis	0.05 (0.01)	0.06 (0.01)	n.s.	0.06 (0.01)	0.05 (0.003)	n.s.
Metritis	0.17 (0.01)	0.20 (0.01)	0.05	0.19 (0.02)	0.18 (0.02)	n.s.
Retained Placenta	0.05 (0.01)	0.06 (0.01)	n.s.	0.05 (0.01)	0.05 (0.01)	n.s.
Milk fever	0.11 (0.01)	0.13 (0.01)	n.s.	0.08 (0.01)	0.13 (0.01)	0.01
Lameness	0.13 (0.01)	0.11 (0.01)	n.s.	0.13 (0.01)	0.11 (0.01)	n.s.
ONO	0.16 (0.01)	0.11 (0.01)	0.001	0.14 (0.01)	0.14 (0.01)	n.s.
FSC	0.39 (0.02)	0.45 (0.03)	0.05	0.41 (0.03)	0.42 (0.02)	n.s.
DFH	52.9 (1.6)	42.0 (1.6)	0.001	44.4 (1.6)	50.6 (1.6)	0.01
CI	395.3 (2.9)	383.5 (2.9)	0.01	389.6 (2.9)	389.3 (2.9)	n.s.
DOP	124.0 (3.3)	106.6 (3.3)	0.001	113.2 (3.3)	117.2 (3.3)	n.s.
DFS	77.2 (1.2)	71.9 (1.2)	0.001	72.3 (1.2)	76.8 (1.2)	0.01

Mastitis and lameness were also coded according to the number of cases occurring in a lactation. The number of cases of mastitis in a lactation ranged from one to seven, with 95% of cows having an incidence of zero or one. Lameness ranged between one and thirteen recorded cases per cow in a lactation, with 81% of recorded records for lameness being zero or one. Lactation number was the only significant effect for mastitis coded from 0-7 and the Wald statistics were of approximately the same magnitude as when mastitis was coded as a 0/1 trait. Year of calving and lactation number were the only factors significantly affecting lameness, analysed as number of recorded incidences per year. This result is consistent with the 0/1 analysis.

Table 4.4 Estimates for regression coefficients of the traits† on pedigree index for kg fat + protein (standard errors (s.e) are approximate)

	b	s.e.
Mastitis	0.088*	0.004
Ketosis	-0.002	0.006
Metritis	-0.003	0.003
Retained Placenta	-0.001	0.004
Lameness	0.004	0.004
ONO	0.013***	0.003
FSC	-0.002*	0.001
DFH	0.402***	0.066
CI	0.485***	0.108
DOP	0.665***	0.127
DFS	0.214***	0.040

† GLMM failed to converge for milk fever, hence no regression coefficient was available.

Regressions of the traits on PI reflect the consequences of selecting bulls for high fat plus protein yields. The regression coefficients are shown in Table 4.4. Regressions of ONO, FSC, DFH, CI, DOP and DFS on PI were all significantly different from zero ($P<0.001$), which agrees with the differences between genetic lines observed in the smaller data set. In addition to these traits the regression of mastitis on PI was also significantly different from zero ($P<0.05$). When the smaller data set (1988-1996) was used, regression coefficients of ONO, FSC, DFH, CI, DOP and DFS on PI were also significant, although the regression of mastitis on PI only approached significance ($P<0.10$).

Heritabilities were also estimated using the larger data set and are shown along with the permanent environmental effects in Table 4.5. The heritabilities ranged from 0.000 for milk fever to 0.149 for DFH.

Table 4.5 Estimates for heritabilities (h^2), additive genetic standard deviations (σ_a) and permanent environmental effects (c^2) obtained from REML VCE. The variances within each lactation were adjusted to one for all health disorders

	σ_a	h^2	s.e.(h^2)	c^2	s.e.(c^2)
Mastitis	0.192	0.038	0.011	0.000	0.000
Ketosis	0.095	0.008	0.010	0.039	0.018
Metritis	0.105	0.012	0.009	0.000	0.000
Retained Placenta	0.134	0.019	0.009	0.000	0.000
Milk fever	0.000	0.000	0.000	0.055	0.011
Lameness	0.255	0.082	0.020	0.071	0.020
ONO	0.004	0.046	0.018	0.009	0.023
FSC	0.114	0.016	0.011	0.015	0.016
DFH	11.3	0.149	0.022	0.028	0.023
CI	13.4	0.085	0.023	0.042	0.033
DOP	19.0	0.126	0.028	0.203	0.037
DFS	6.8	0.128	0.022	0.054	0.026

4.4 Discussion

Most studies on genetic aspects of health and fertility traits have been based on large data sets from field records, but with a relatively limited number of traits (e.g. Uribe *et al.*, 1995; Chapter 2). Few studies have investigated the range of health and fertility traits included in the present study. The analyses described here were based on fewer records, but included a more comprehensive range of traits, many of which are not currently recorded in national recording schemes. This is especially true for the health disorders - in the present study six different health disorders were considered.

The two genetic lines investigated here formed part of an experimental research herd, consequently there were no management biases favouring one line above the other. Therefore, differences between the two lines on the same diet were therefore unaffected by management decisions. Significant differences between the two lines were observed for the fertility traits, but not health traits. The regressions of the health and fertility traits on PI confirmed this. At present, over 20 years of selection for fat plus protein yield in this herd appears to have resulted in a deterioration in fertility, but not in health traits; although there was a small, but significant positive regression of mastitis on PI (Table 4.4). Jones *et al.* (1994) compared the incidence of health disorder in a genetic selection line, selected for PTAs for milk yield, and a

control line, and found significantly higher total health expenses, mastitis, edema and leg problems in the selection line.

Many of the fertility traits used in our study were related. For example, if a cow is not seen in oestrus, and hence has ONO recorded as 1, it might be expected to have a longer DFH and DFS than a cow where ONO is coded as 0. Furthermore, a delay in DFH and DFS may result in a longer DOP and CI. Consequently, similar fixed effects were important for all the fertility traits (Table 4.1) and genetic correlations between similar fertility traits have been found to be high in larger data sets (e.g. Chapters 2 and 3).

Most health disorders analysed here increased significantly with increasing parity, which confirmed results from preliminary studies using Langhill data (e.g. Nielsen *et al.*, 1997b). McGowan *et al.* (1996) investigated three fertility measures in 364 Langhill heifers and cow lactation records, and found that reproductive performance was poorest in heifers on the high concentrate feeding system. Parity effects were not significant for the fertility measures in the present study, except for FSC ($P<0.01$) which was highest in second to fourth lactation animals (Table 4.2). MacMillan *et al.* (1996) argued that the main effect of lactation on fertility in dairy cattle is between lactating cows and younger non-parous heifers, with levels of fertility lower among lactating cows than non-parous heifers. The extent of this difference was less in pasture fed cows in New Zealand (<10%) than in American Holsteins (>20%).

Feeding system significantly affected DFH, DFS and milk fever. All cows were fed the same diet in the dry period, so the effect of feeding system on milk fever was unexpected as this disease is peri-parturient. Milk fever (hypocalcaemia) is associated with a fall of blood calcium levels, which is a consequence of insufficient uptake of calcium from the diet at around the time of calving. As most cows get milk fever in their third, or subsequent lactations, it is possible that there is a carry-over effect of the diet in previous lactations. DFH and DFS are closely related traits, and the observed dietary effects on these traits are likely to be for the same reasons. The

peak nutrient requirement of the mammary gland is within the first ten weeks of lactation. If the cow partitions too much of her nutrients towards milk production, reproduction is likely to suffer. Veerkamp *et al.* (1995b) observed significant differences between the two feeding systems for dry matter intake. Poor reproductive performance on the LC diet may therefore be affected by problems of matching nutrient requirements to nutrient intake. Furthermore, work on residual feed intake (RFI; actual ME requirement minus estimated ME requirements) in this population of cattle by Veerkamp and Emmans (1995) have shown that cows have a negative RFI early in lactation, and this is particularly marked in S cows fed the low concentrate food.

Means for 0/1 traits estimated using GLMM were very similar to means estimated using REML. This was expected as variances, but not means, are affected when normal distributions are assumed for 0/1 traits. The heritability estimates of most traits were small in the present study, which is consistent with heritability estimates from the analyses of field data presented in Chapters 2 and 3. However, the heritability estimates of DFH, DOP and DFS were between 0.12 and 0.15 and genetic variances were also reasonably large. Therefore, it may be possible to effect sizeable improvements in at least one of these traits in a breed improvement programme. DFH, DOP and DFS are related traits; cows with longer DFH and DFS are expected to also have a longer DOP. Genetic correlations between DFH, DOP and DFS were high (not presented here). Consequently, these could be different measures of the same trait.

4.5 Conclusions

Selection on PTAs for fat plus protein seems to have led to a deterioration in the measures of fertility used here. This does not appear to be true for the health disorders in this study, with the possible exception of mastitis. However, most studies on national data have indicated a deterioration in some health traits as a consequence of selection for milk yield. Hence, investigation of more comprehensive breeding goals to include health and fertility traits is warranted. There was no genetic

line by feeding system interaction, indicating the effects of selection for fat plus protein on health and fertility appear to be similar, whether cows are fed relatively high or relatively low levels of concentrates in a complete mixed ration. In countries such as the UK, which import a high proportion of semen from countries where bulls are tested in generally high input systems, it is important to check for the presence of G x E interactions periodically.

Chapter 5

Expected correlated responses in breeding programmes that include production, health and fertility

5.1 Introduction

The aim of most dairy genetic improvement programmes is to change the genetic merit of animals, so that future generations will produce milk more efficiently under the prevailing economic and social circumstances. In the past, breeding goals were mainly concerned with increasing yields of milk and its components. However, profit is affected by other characteristics, such as fertility, health, longevity, feed intake and feed efficiency. Including some of these in the breeding goal may increase overall efficiency and profitability by reducing inputs relative to outputs.

The most compelling reason to incorporate health and fertility traits into a selection index for overall genetic merit is because there is general agreement in the literature that selection for production appears to have led to a deterioration in health and fertility traits. Genetic correlations between production and fertility traits are in most cases unfavourable and range between 0.22 and 0.65 for interval traits and are around -0.25 for conception rates (Chapter 1, Chapter 2 and Chapter 3). Genetic correlations with mastitis and lameness have also been found to be antagonistic (Chapter 1, Chapter 2 and Chapter 3). Although heritability estimates for health and fertility traits are low, typically less than 10%, it has been argued (Jansen, 1985; Emanuelson, 1988) that there is sufficient genetic variation to make genetic progress. The low heritabilities may be explained by the large influence of environmental factors.

There are several ways to measure fertility including calving interval, days open, and conception and non-return rates. Obviously these traits are related, but currently there is no single universally accepted measure. Maintaining calving intervals of high-producing cows is an important management objective in many herds (Esslemont,

1995). Therefore, in this study, calving interval was chosen as the measure of fertility. Mastitis and lameness were considered, as they are economically the most important diseases (Kossaibati and Esslemont, 1997).

In the UK there is no nationally-organised recording scheme for mastitis and lameness, although health disorders are recorded in Scotland by Scottish Livestock Services Ltd (SLS) and in some herds in England and Wales by the Dairy Information System (DAISY). A reduction in the incidence of mastitis is possible by selection for lower somatic cell counts in milk (e.g. Strandberg and Shook, 1989; Philipsson *et al.,* 1995). Many more herds in the UK record somatic cell count (SCC) than mastitis and PTAs are available for SCC, making it feasible to select indirectly for mastitis resistance.

Selection indices have been used extensively in animal breeding to combine traits of economic and biological importance. Most indices used in national dairy cattle breeding programmes require economic values for each trait in the goal in order to give the correct weighting to each trait in the index. Groen *et al.* (1997) gave a comprehensive review of methodology for deriving economic values of functional traits. They advocated that economic values should be calculated according to the production circumstances of the country concerned, which may be affected by legislation on animal welfare, milk quota or pricing levels. In some circumstances it may be inappropriate to apply a single economic value for a trait across the population. For example, Veerkamp *et al.* (1997) considered the economic benefit of reducing SCC according to the milk payment scheme in the UK and suggested that as herds differed in their mean bulk tank samples it was appropriate to assign an economic value for each band, rather than a single economic value for SCC across the whole population. Furthermore, the heritability, sign of the correlation and economic importance of one trait in the goal may be much greater than another, making progress in both traits impossible using an economic index.

There are however alternatives to using economic values to help determine weights for selection indices. For example, desired gains indices are used to obtain genetic change according to a predetermined goal. This type of approach is particularly useful when economic weights for (some) traits in the index are difficult to calculate. A restricted index approach has been discussed as a way to limit genetic change of certain traits in the index to zero (e.g. Brascamp, 1984). Continued deterioration of health traits may be considered to be unacceptable by legislators in the future, which may arise as a response to public opinion on animal welfare. Poor fertility may also be thought of as a welfare consideration. Although in most cases of low fertility there is no perceived direct suffering to the animal, low fertility may be an indicator of metabolic load or of other health problems. Also, failure to conceive has been reported to be the predominant reason for culling in UK dairy cattle (Esslemont and Kossaibati, 1997).

The objectives of this study were (i) to predict the outcome of continuing to exclude health and fertility from the breeding goal, (ii) to investigate the consequences on milk, butterfat and protein yields when health and fertility traits were restricted to zero genetic change, and (iii) to investigate an index where the goal is total profit and calving interval, mastitis and lameness are included with a range of economic values.

5.2 Material and Methods

Simple means of the genetic parameter estimates for milk, butterfat and protein yields, calving interval, mastitis, lameness and SCS from Chapters 2 and 3 were used in the present study (Table 5.1). Parameter estimates for SCS were available from DAISY data only, as were correlations between butterfat and protein yields and the health and fertility traits (Chapter 3).

Table 5.1 Means, phenotypic standard deviations (σ_p), genetic standard deviations (σ_a), heritabilities (along the diagonal), genetic correlations (below the diagonal) and phenotypic correlations (above the diagonal)

Trait	MILK	BFAT	PROT	CI	MAST	LAME	SCS
Mean	6594 kg	260 kg	209 kg	385 d	0.12	0.10	3.25
σ_p	1075 kg	45 kg	36 kg	45 d	0.28	0.28	1.07
σ_a	618 kg	23 kg	19 kg	7.1 d	0.067	0.053	0.41
1. Milk yield (MILK)	**0.33**	0.69	0.71	0.20	-0.01	0.04	-0.08
2. Butterfat yield (BFAT)	0.92	**0.27**	0.73	0.16	-0.02	0.01	-0.10
3. Protein yield (PROT)	0.99	0.96	**0.27**	0.16	0.02	-0.01	-0.10
4. Calving interval (CI)	0.39	0.53	0.36	**0.025**	0.04	0.04	0.12
5. Mastitis (MAST)	0.26	0.27	0.29	0.11	**0.057**	0.05	0.23
6. Lameness (LAME)	0.17	0.12	0.13	0.20	0.33	**0.036**	0.04
7. SCS	0.16	0.11	0.14	0.28	0.65	0.26	**0.15**

It was assumed that all index traits were predicted transmitting abilities (PTAs) from a complete multivariate best linear unbiased prediction (BLUP) i.e. that the PTAs were known without error. Partial regressions were calculated from estimated genetic variances and covariances:

$$R = G^{-1}G_{ig}$$

where R is a matrix of partial genetic regression coefficients of m goal traits and n index traits and the matrix G_{ig} (n x m) contains the genetic covariances between the index and goal traits. The G matrix is symmetric (n x n) and is the genetic (co)variance matrix between the PTAs of the index traits. Prior values of the (co)variance matrices were checked to ensure that these matrices were positive definite. Negative eigen values were set to 10^{-7}. The optimal index weights (b) were the sum of the partial genetic regression coefficients of goal traits on index traits (Veerkamp *et al.*, 1995a): $b = Rv$ where v is the vector of economic weights.

Matrices for the restricted index, NG_{ig} and NG, were constructed from the G_{ig} and G matrices, modified from Cameron (1997):

$$NG=\begin{bmatrix} G & G_{ig1} \\ G'_{ig1} & M0 \end{bmatrix} \qquad NG_{ig}=\begin{bmatrix} G_{ig} \\ M0 \end{bmatrix}$$

NG included the G matrix and extra columns and rows from G_{ig} that corresponded to k restricted traits, G_{ig1} (n x k), and a k x k matrix consisting of zeros (M0). NG_{ig} was constructed using G_{ig} and an m x k matrix of zeros (M0). Economic weights from

Veerkamp *et al.* (1995a) were used. These estimates were based on assumptions for the future UK milk price and were £-0.03, £0.60 and £4.04 per kg of milk, butterfat and protein respectively. Selection index equations were used to evaluate the consequences of selection for the breeding programmes (BP) outlined in Table 5.2. Milk, butterfat and protein yields were included in all breeding programmes. In all cases it was assumed that relationships between traits were linear.

Table 5.2 Characteristics of breeding programmes

Breeding Programme (BP)†	Goal: MILK+BFAT+PROT+	Index: MILK+BFAT+PROT+	Traits restricted:
1	-	-	-
2	CI	CI	CI
3	MAST	MAST	MAST
4	LAME	LAME	LAME
5	CI+MAST+LAME	CI+MAST+LAME	CI+MAST+LAME
6	SCS	SCS	SCS
7	MAST	SCS	MAST
8	MAST	MAST+SCS	MAST

†MILK, BFAT and PROT were included in the goal and index of all breeding programmes

In the indices considered initially, it was assumed that the economic values of health and fertility traits were unknown. There is some justification in using this approach, in that restricting health and fertility to zero genetic change may be a desirable goal from a welfare perspective. Moreover, economic values for health and fertility traits are difficult to estimate as they are affected by a plethora of factors which may vary in their impact on the trait considered. For example, fertility is influenced by many management factors, among which insemination decisions are affected by the seasonal pricing structure for milk, quota restrictions, desired replacement rates etc.

Another strategy to avoid this problem of deriving economic values is to use several different levels of economic values for calving interval, mastitis and lameness. In most circumstances selection indices are robust to large changes in economic values. Veerkamp *et al.* (1995) changed the economic value of longevity by 1.5 and 2 fold and found that this had only a small effect on the efficiency of their index. However, the possible range of economic values for health and fertility traits may be much greater than those for production traits and the assumptions involved less robust. For

example, based on work by Esslemont and Peeler (1993) and Stott *et al.* (1997), the economic value of calving interval is between £3 and £10 per day.

Few attempts have been made to derive economic values for mastitis and lameness for animal breeding purposes. Kossaibati and Esslemont (1997) estimated that the average direct cost of mastitis per cow per lactation was £153. However, the latter figure includes only direct costs associated with treatment and indirect costs, such as the cost of discarded milk etc. There may be justification in increasing the economic value given to mastitis (and lameness), to account for other benefits, e.g. fewer premature culls, improved animal welfare. When costs associated with risk of culling and fatality were included, the average cost per average affected cow per lactation was calculated to be £218 (Kossaibati and Esslemont, 1997). So there may be justification in using a large economic weight for mastitis. Accounting for public opinion in economic values presents a major challenge. Bennett (1995) argued that peoples' perceptions of what is and is not an acceptable level of animal suffering vary and the boundaries are changeable. Also deriving an economic value to reflect this presents major difficulties. This issue is discussed further by Bennett (1995). However, public concern on welfare may mean that the economic values at the upper end of the range presented here should be considered.

Finally, while it may be feasible to use a multivariate approach to obtain PTAs for milk production, health and fertility the assumption that PTAs are known without error may be unrealistic. This may be a particular problem for PTAs with low accuracies, such as health and fertility traits. This may result in an over-emphasis of these traits in an index designed to maximise profit. Therefore, using genetic and phenotypic correlations between traits and their phenotypic standard deviations, a P matrix was constructed as the (co)variances between PTAs for index traits, assuming a typical progeny test scenario of 100 daughters per sire. Responses were calculated as:

$$R = P^{-1}G_{ig}$$

Table 5.3 Optimum index weights for the breeding programmes

	Breeding programme (BP)							
Index:	1	2	3	4	5	6	7	8
PTA for:								
MILK (kg)	-0.03	-0.03	-0.03	-0.03	-0.03	-0.03	0.10	-0.03
BFAT (kg)	0.60	0.60	0.60	0.60	0.60	0.60	1.39	0.60
PROT (kg)	4.04	4.04	4.04	4.04	4.04	4.04	-1.41	4.04
CI (days)	-	-3.90	-	-	-3.68	-	-	-
MAST	-	-	-252	-	-218	-	-	-258
LAME	-	-	-	-152	-20.0	-	-	-
SCS	-	-	-	-	-	-17.8	-55.0	0

Weights for the production index, BP1 (and all the other indices except for BP7) were equal to the economic values of each of the yield traits (Table 5.3), as expected when multivariate BLUP PTAs are used. Using the methodology described for the restricted index it is possible to estimate economic values (dummy values) for those traits restricted in the index. For all indices except BP7, the dummy value is equal to the negative of the index weight of the restricted trait in the goal. For example, the derived economic value for mastitis in BP8 is £258 per affected lactation. If the index differs from the goal, e.g. when mastitis was restricted to zero in an index that included production and SCS (BP7), then the dummy value is equal to the assumed economic weight for the trait in the goal. For BP7 the dummy value was £442. The index weight for lameness was -152 in the index to restrict lameness to zero change (BP4), when calving interval, mastitis and lameness were restricted to zero change in the goal (BP5) the weight on lameness was reduced to -20.0. This is because mastitis and calving interval partly predicted lameness, correlations between these three traits being positive in sign.

Weights for calving interval, mastitis, lameness and SCS were sensitive to small changes in heritabilities and genetic correlations, and should therefore be treated with caution. Responses to selection were much more robust to slight changes in parameter estimates.

Table 5.4 Predicted consequences of one standard deviation of selection in units of measurement and for overall economic response (H) for the investigated breeding programmes, assuming PTAs are known without error

Index:	1	2	3	4	5	6	7	8
MILK (kg)	600	552	582	590	538	592	569	582
BFAT (kg)	22.9	19.6	22.0	22.7	19.0	22.7	21.4	22.0
PROT (kg)	18.7	17.4	18.0	18.5	16.9	18.5	17.6	18.0
CI (days)	2.78	0	2.71	2.62	0	-	-	-
MAST	0.018	0.017	0	0.017	0	0.013	0	0
LAME	0.007	0.003	0.005	0	0	-	-	-
SCS	-	-	-	-	-	0	-0.084	-0.031
H (£)	71.3	65.5	68.8	70.6	63.5	70.7	66.9	68.7

Selection responses for the eight breeding programmes are shown in Table 5.4. One standard deviation of the index is equivalent to selecting the top 16% of males. When selection was for yield only (BP1), calving intervals were expected to increase by 2.78 days per unit selection differential. The incidence of mastitis and lameness were also expected to rise by 0.018 and 0.007 cows with one or more cases of mastitis and lameness respectively. BP2, designed to restrict calving interval to zero genetic change, had the greatest impact on the milk production traits (when only one trait in the index was restricted). Restricting mastitis and lameness to zero change (BP3 and BP4) had less effect on the production traits, although the non-restricted index (BP1) shows sizeable changes in the incidence of both mastitis and lameness. Although the index weights for BP7 were different from the optimum index weights for production (Table 5.3), there is little change in the actual responses to selection for production traits (Table 5.4). Restricting SCS to zero change (BP6) would still cause an increase in mastitis, but the rate of genetic change in mastitis would be less than when health and fertility traits were excluded from the breeding goal (BP1). Using SCS to restrict mastitis to zero change would result in a substantial change in SCS of -0.084.

Table 5.5 Predicted consequences of selection on BP1 and BP5 in units of measurement for (a) production traits and (b) health and fertility traits in a hypothetical progeny testing scheme, assuming 100 daughters per sire

		BP1	BP5
Change in index (s.d.)		0.22	0.22
a	H (£)	15.7	14.0
	Milk yield (kg)	132	118
	Butterfat yield (kg)	5.0	4.2
	Protein yield (kg)	4.1	3.7
b	Calving interval (days)	0.61	0
	Mastitis	0.004	0
	Lameness	0.002	0

Table 5.5 shows examples of expected responses to selection when selection intensities corresponding to a hypothetical progeny testing program are considered for BP1 and BP5. Assuming that a change of 0.22 standard deviations in the index approximates the annual selection response in a four pathway breeding scheme, annual economic responses for selection on BP1 and BP5 are £15.6 and £13.9 respectively, equivalent to an 11% reduction in economic response, although this does not account for the benefits of decreased incidence of disease and of improved fertility.

Table 5.6 Expected responses to selection using three levels of assumed economic values for calving interval, mastitis and lameness

	Breeding programme		
	9	10	11
Economic values (£):			
Calving interval (£/d)	3	5	8
Mastitis (£/lact)	50	100	300
Lameness (£/lact)	50	100	300
Responses:			
H (£)	65.1	65.3	74.4
Milk yield (kg)	567	503	326
Butterfat yield (kg)	20.5	17.4	10.1
Protein yield (kg)	17.9	16.0	10.7
Calving interval (d)	0.60	-1.06	-3.31
Mastitis	0.01	0.00	-0.01
Lameness	0.00	0.00	-0.02

Table 5.6 shows expected responses when an index using multivariate BLUP PTAs is used to optimise the economic response assuming low, medium or high economic values for calving interval, mastitis and lameness. Obviously a greater response in

the health and fertility traits is achieved when the economic values of these traits become larger. Even when the economic values of the health and fertility traits are large, the magnitude of selection responses are comparatively higher for production traits than health and fertility traits. This is because production traits have high heritabilities and economic values, there are high positive correlations between them and there are unfavourable correlations between the milk production traits and health and fertility traits.

Table 5.7 Expected responses to selection assuming each sire has 100 daughters and there are three levels of assumed economic values for calving interval mastitis and lameness

	Breeding programme		
	12	13	14
Economic value (£)			
Calving interval (£/d)	3	5	8
Mastitis (£/lact)	50	100	300
Lameness (£/lact)	50	100	300
Responses			
H (£)	63.0	62.5	67.0
Milk yield (kg)	576	525	358
Butterfat yield (kg)	20.7	18.0	10.9
Protein yield (kg)	17.9	16.4	11.3
Calving interval (d)	1.15	-0.23	-2.36
Mastitis	0.01	0.0	-0.01
Lameness	0.0	0.0	-0.01

The expected responses in health and fertility traits when each sire is assumed to have 100 daughters (Table 5.7) are lower than when the PTAs are assumed to be known without error (Table 5.6). The main reason for this is because, with only 100 daughters, the reliabilities for the PTAs would be lower for calving interval, mastitis and lameness than for the production traits.

5.4 Discussion

Selection for production traits alone was expected to result in longer calving intervals and more cases of mastitis and lameness. Restricting the index to no genetic change in calving interval, mastitis and lameness caused a moderate reduction in overall economic response in production, equivalent to 11% of the response in PIN. However, this ignores the economic benefit of preventing a decline in genetic merit

for health and fertility. However, it is possible that pressure from public opinion would make restricting genetic change in health and fertility to zero realistic. When an index to optimise economic responses is used calving interval, mastitis and lameness would continue to deteriorate, albeit at a slower rate than BP1, unless they are assumed to have large economic values (BP11). Strandberg and Shook (1989) concluded that simultaneous improvement of both yield and mastitis resistance was not economically desirable due to the positive correlation between traits and the higher heritability and economic value of milk production compared to mastitis.

Derivation of reliable economic values for health and fertility traits is necessary to optimise economic response of the aggregate genotype, as an economic index should always at least equal, but usually out-perform, a constrained index.

In the UK longevity has been incorporated into the breeding goal of one of the indexes available (ITEM; Veerkamp *et al.,* 1995a). In this study longevity, or survival, was defined as the probability that a cow reaches her fourth lactation. It is clearly unfeasible to delay selection until progeny tests on bulls based on actual records of survival are available, so longevity is predicted initially mainly from linear type traits (plus ancestral information), and eventually from a combination of type traits and actual longevity data where available. Survival is obviously related to health and fertility traits; important reasons for premature culling in dairy cattle include failure to conceive, mastitis and lameness (Esslemont and Kossaibati, 1997). However, the main reason why more countries consider longevity than health and fertility, as a selection objective is that health and fertility are either not recorded, or evaluations are unavailable. However, the Scandinavian countries have recorded and evaluated health and fertility for many years. All four Scandinavian countries include production, growth, conformation, temperament, stillbirth, health and fertility in their selection indices (Philipsson *et al.,* 1994).

The linearity of the relationship between production, health and fertility traits is an area that should be investigated in future research. If the relationship is non-linear

then, for example, a small reduction in the response in production may cause a large reduction in calving interval, mastitis or lameness. Philipsson *et al.* (1995) found a positive linear relationship between mastitis and SCC, indicating that lower cell counts would reflect a reduced incidence of mastitis rather than reduced ability to combat them.

For mastitis and lameness in particular, it may be advantageous to use predictor traits as selection criteria in addition to, or instead of, recording clinical cases in a progeny testing scheme, as they are generally easier to measure and record and have higher heritabilities. Feet and leg traits (e.g. linear type scores) and locomotion measurements may be suitable characteristics for incorporating into a breeding programme to reduce the incidence of lameness (Boelling and Pollott, 1997). A suitable candidate trait for predicting mastitis is SCS as it is widely recorded in many countries and has a reasonably high correlation with clinical mastitis and a higher heritability (Chapter 1, Chapter 3). Some aspects of udder conformation are also believed to be related to mastitis resistance (e.g. Lund *et al.*, 1994) and may be used as selection criteria for mastitis resistance, most likely in addition to SCS. In the present study SCS was found to be useful as a selection criterion to restrict mastitis to zero genetic change, however this led to a change in index weights for the production traits. When SCS and mastitis were both used in an index, SCS was redundant and consequently had no weight in the index. This was because SCS has already contributed to the PTA for mastitis in a complete multivariate BLUP approach. However, SCS may have particular value in a breeding programme to improve mastitis resistance when progeny group sizes are small. Using an index with SCS and mastitis, Philipsson *et al.* (1995) predicted that the relative importance of SCS in a breeding programme to improve mastitis resistance was greater when progeny groups were small.

National indices are useful as a selection tool for dairy farmers, because they enable animals to be ranked in 'league tables' and thus make bull selection in particular a simpler task. An alternative to national selection indices is customised indices. These

are based on the same principles of economic indices, but are tailor-made to suit individual farm or group circumstances (Visscher and Amer, 1996). There are several reasons why it might be preferable to have selection indices calculated on a farm rather than a national basis: in particular different farm sizes, levels of intensity of farming and pricing strategies by milk buyers, which may include financial penalties for poor health and welfare.

5.5 Conclusion

There is considerable pressure to incorporate health and fertility traits into dairy cattle breeding goals to counter the apparent deterioration in these traits with increasing milk production. Although annual changes in health and fertility may seem small they accumulate to significant amounts. However, using a breeding goal constrained to no genetic change in health and fertility traits would have an economic impact on returns from milk production. Deriving economic weights for health and fertility traits is necessary to optimise economic response of the aggregate genotype, but a continued deterioration in health and fertility is still likely. Future breeding programmes should perhaps consider compromising genetic improvement in production for a more balanced goal, including improved disease resistance, better fertility and production.

Chapter 6

General Discussion

6.1 Introduction

In this study, genetic parameters for milk, fat and protein yields and a range of health and fertility traits were estimated, using field data from two recording schemes (Chapters 2 and 3). In addition to this, data from the Langhill Dairy Cattle Research Centre were used to evaluate the consequences of selection solely for butterfat and protein yield on dairy cow health and fertility, and to investigate whether a genetic line by diet interaction exists for these traits (Chapter 4). Responses to selection were predicted for several hypothetical breeding programmes (Chapter 5) using the genetic parameters estimated in the studies reported in Chapters 2 and 3.

At present, few countries record and estimate breeding values for health and fertility traits in their national breeding programmes. The Scandinavian countries are among those that do, and there is interest in many other countries to follow their lead and expand breeding goals to include health and fertility. There are several compelling reasons for doing this, including the apparent unfavourable relationship between some of these traits and milk production, effects on profitability and also ethical and welfare implications.

Dairy cattle breeding is already very much on a global scale, with many of the most popular sires being used as AI sires across the world. Relatively few breeding companies have progeny testing schemes of sufficient size to produce proven bulls of world class calibre consistently. Thus, decisions regarding the choice of parents of future bulls rests firmly in the hands of a few. A demand for genetic evaluations of health and fertility traits will inevitably mean that progeny testing schemes will need to consider either direct recording of these traits or basing predictions on information from other sources, such as correlated traits or information from relatives in countries

with health recording. If direct recording is chosen, then in order to achieve reasonable accuracies of selection, progeny group sizes would need to be relatively large. For example, in Norway, where mastitis and ketosis are included in the breeding goal, the average progeny group size is 200 (Solbu and Lie, 1990). In the SLS and DAISY data sets only 19 and 6 sires respectively had 200 or more daughters. In some respects small daughter groups in both these data sets should be expected, as the data represents only a small proportion of milk recorded herds. In order to obtain direct evaluations for health and fertility traits in the UK, much more reliable health and fertility data needs to be available. This can be achieved either by more extensive use of the national recording schemes, or by concentrating recording in those herds involved in progeny testing.

The intention in this chapter is to provide a synthesis of the main points from the previous chapters in the context of future UK breeding goals that include health and fertility traits. The results presented in the preceding chapters are by no means conclusive in terms of what traits should be included as breeding goal traits and selection criteria, but important issues have been raised in particular:

i) Possible strategies for recording health and fertility information.

ii) The relationship between health and fertility traits and production traits.

iii) Appropriate selection criteria for health and fertility traits.

In addition, areas of future importance are also discussed including international evaluations of health and fertility and further areas for research.

6.2 Recording schemes for health and fertility

Collecting and using data is the basis of practical breeding schemes. Information on identity, pedigree and performance records for each animal are required to: i) help define future breeding goals through genetic and phenotypic parameter estimates for goal traits and index measurements; and ii) identify and select the best animals as parents of the next generation.

There are three regional milk recording agencies in the UK. By far the largest is the National Milk Records (NMR) which operates mainly in England and Wales and accounts for around 87% of dairy cows in the UK (National Dairy Council, 1997), the Scottish Livestock Services (SLS) record approximately 8% and the smallest is the United Dairy Farmers (5%). All three recording agencies record milk yield, butterfat percentage, protein percentage and somatic cell counts. Most of these recording schemes also collect details of inseminations for management purposes and to provide parentage information for the resulting offspring. However, to date, only SLS record health disorders.

Details of health, culling and service events occurring on each farm are collected monthly by SLS. In order to encourage as many farmers as possible to record this information, there is no charge for this service. However, to ensure consistent recording of health disorders there has to be some benefit or reason for recording. One such benefit could be to identify potential cull cows, but most farmers tend to 'know' which cows are persistently mastitic, etc. A more compelling reason (and one of the reasons why the scheme was initially set up) would be if welfare-assured schemes demanded this type of information; all milk buyers in Scotland employ representatives to check on farm welfare and hygiene practices. However, if there are penalties for high incidences of health disorders, then this may encourage deliberate under-recording.

The other source of field data used in this study was recorded by the Dairy Information System (DAISY; Chapter 3). DAISY is a computer based recording scheme available to all UK farmers and veterinary practices (although most participants are in the South of England). Information on health and fertility is used to assist in management strategies, such as culling decisions and veterinary fertility check-ups. More recently it has expanded to include production traits. Farmers recording with DAISY are aware that recording health disorders and service information can be useful as a management tool and are prepared to pay for this service. As a consequence, fewer farms record with DAISY than SLS, so in some

ways there is a trade-off between recording detail and the numbers of records available. Of course the greatest level of detail in terms of recording categories is found in data from research herds, such as Langhill. However, genetic parameter estimation using data from just one herd has limitations, as records are from relatively few cows, even when the data cover many years.

Although the traits analysed were similar in both SLS and DAISY data sets, the nature of the recording schemes were in some respects quite different. SLS record commercial dairy herds and the main priority of their scheme is to collect milk production records. DAISY is operated by veterinarians and farmers as a health and fertility monitoring scheme.

The incidences of mastitis and lameness were lower and conception rates better in SLS data than DAISY data, which is probably a consequence of under-recording rather than a better health and fertility status in SLS herds. However, although heritability estimates were small (less than 0.1 for all health disorders and fertility traits), they agreed well between the two recording schemes. In addition to this, many of the correlation estimates were similar in both SLS and DAISY data sets. This implies that the nature of the recording scheme had little effect on the parameter estimates obtained. This was surprising, as under-recording in SLS herds might have resulted in a larger error variance than that in parameters from the DAISY scheme (and consequently lower heritabilities). However, when traits are largely controlled by non-genetic effects (and as a result heritabilities are small), differences due to the recording scheme may be expected to be small. Furthermore, similarities between estimates may have arisen due to chance. Nevertheless, the main conclusion here, is that simple schemes do not necessarily give poorer results, as far as a genetic evaluations are concerned. This should encourage other UK recording schemes to adopt even simple health recording schemes.

The simplicity of the SLS recording scheme has advantages and appears to be quite effective compared to other more complicated schemes. However, computer based

schemes, such as DAISY, have various merits. Although probably not of immediate importance, it is worth considering benefits of computerised schemes, for recording health and fertility information. More farms than ever before have their own computers and technology such as electronic transfer of data is convenient and offers good opportunities to reduce human (typing) errors in recording. In some respects recording in this way is simpler, and thus more farmers may take advantage of software designed to record health events. Data entry may become more consistent if farm staff use the computers routinely e.g. on a daily basis. However, there is a risk that farmers may see little benefit in sending their data to a recording agency, as they can store and produce all the information they require at home. Clearly this would create immense problems for routine genetic evaluations.

At present too few herds in the UK record information on health disorders to make routine genetic analyses feasible. Farmers already recording with DAISY and SLS will continue to provide invaluable information on health and fertility. However, for the purposes of developing breeding goals and producing genetic evaluations, more records on this type of information would be needed. In Norway 87% of all herds participate in the national health recording scheme (Ruane *et al.,* 1997). There are various reasons for such widespread involvement in the Norwegian scheme, but perhaps the most important is that veterinarians are responsible for recording health disorders.

In the UK, perhaps the best opportunity to expand health recording would be inclusion of herds participating in progeny testing schemes. Records on daughters of progeny test sires and their (herd) contemporaries could be collected and used for routine genetic evaluations. Costs associated with recording health and fertility information in progeny testing schemes could either be supported by a levy on milk sales paid by all producers, or funded directly from the breeding companies. Of course, it is likely to be the producer who ultimately pays, either through higher semen costs or direct levies.

The key to improving the quality of health and fertility data in the UK is to prove its usefulness, for example by providing genetic evaluations for some health and fertility traits. Many farmers in Scandinavian countries are already convinced of the benefits of breeding for improved health and fertility (e.g. Philipsson *et al.*, 1994; Ruane *et al.*, 1997). There are other direct benefits, in particular aiding management decisions such as identifying potential culls. In addition to this, there are several spin-offs including monitoring trends in fertility and the most important diseases, which is currently done using DAISY data (e.g. Kossaibati and Esslemont, 1995), but not on a national scale. As data collected by SLS accumulate, trends in Scotland can be monitored.

6.3 Relationship between production traits and health and fertility

Selection for milk and its components has led to a decline in fertility in UK dairy cattle (Chapters 2, 3 and 4). In the studies reported in Chapters 2 and 3, genetic correlations between health traits and production were also unfavourable. Results from Langhill (Chapter 4) showed no statistically significant differences between genetic control (C) and selection (S) lines for health disorders. A possible exception to this was mastitis, as the regression of mastitis on pedigree index (PI) was positive in sign and significantly different from zero ($P<0.05$). One of the advantages of using data from a research herd, such as Langhill, rather than field data, is that differences arising from genetic selection can be detected as management effects are removed. S and C lines are fed, housed and managed in identical ways. There is, therefore, little risk of preferential treatment of cattle of high genetic merit. In the literature, correlations between production and fertility traits, in particular, are often thought to be biased upwards as high genetic merit cows are believed to be given longer between calving and first service and more opportunities to conceive (e.g. Philipsson, 1981). However, the results presented here firmly suggest that high genetic merit cattle have poorer fertility.

Non-significant differences between Langhill S and C lines for the health traits appear to support the belief that good management, nutrition and housing can help

control these disorders, although the significant regression of mastitis on PI is cause for concern. In the analyses of field data, moderate, but unfavourable, relationships between production and health traits may have arisen because management and nutrition of cows of high genetic merit within some of these herds is not as good as at Langhill. Indeed Langhill can, in some respects, be managed better than commercial herds, because detailed information is available, e.g. on daily food intake records. Other practices on the farm may also contribute: for example, the introduction of routine foot trimming at Langhill reduced the incidence of lameness and could be a reason why there were no differences between S and C lines for lameness; moderate antagonistic correlations between production and lameness were found in the field data studies.

The unfavourable relationship between production and fertility could be partly due to a mismatch between nutrient requirements and availability in early lactation, resulting in an energy deficit (negative energy balance or metabolic load). This deficit may be reconciled by body tissue mobilisation. Although most mammals are in a negative energy balance early in lactation, it is the magnitude and duration of the deficit that is critical (Nielsen and Lawrence, 1996). If it is large, then in an attempt to sustain lactation, health and fertility may suffer. Fertility is a particular problem, as re-breeding coincides with peak metabolic load. Measuring energy balance is difficult, but some traits related to food intake and tissue mobilisation in early lactation may be used as approximate measures; examples include dry matter intake, live weight and condition score. Estimates of correlations between these traits and health and fertility traits may help to elucidate the role of energy balance.

In the future, increases in yield on lower input diets, as a result of continued selection on higher input diets, may be limited by body tissue mobilisation. In the study reported in Chapter 4, however, differences in health and fertility between Langhill S and C lines on the two diets were non-significant, i.e. there were no significant diet by genetic line interactions (G x E). It is possible that the two diets were too similar to detect differences in performance between S and C lines. However, as genetic

merit of the selection line increases, genotype by environment interactions for these traits may emerge, therefore monitoring should continue periodically.

6.4 Selection criteria for health and fertility

6.4.1 Fertility

The unfavourable relationship between milk production traits and measures of fertility in all three data sets raises the question of whether traditionally accepted calving intervals of 365 days are appropriate for high yielding dairy cattle. Average calving intervals of 365 days are very important where milk production is closely dependent on pasture growth pattern e.g. in New Zealand (Grosshans *et al.,* 1997). In much of Europe and North America, however, cows are housed and therefore fed diets based on silage for part of the year, so there is less pressure to maintain 365 day calving intervals. As a consequence, many farms now have cows calving all year. If longer calving intervals are profitable, then perhaps the best measures of fertility are fertility scores, in particular non-return rates and conception to first service. Longer calving intervals as a consequence of a delayed first insemination date may be acceptable, but not as a consequence of failure to conceive to the first or second insemination.

In the studies reported in Chapters 2 and 3, fertility measures were calculated only for records with two consecutive calving dates, so conception to first service was analysed rather than non-return traits. Therefore, these data sets were censored as only cows surviving at least one lactation were included. Censored data may lead to biased parameter estimates, as cows with the poorest health and fertility may be culled and therefore excluded from the data. However, for non-return traits incomplete information may also lead to biases. In the SLS data set (Chapter 2) many records were lost as the calculated gestation length exceeded 20 days either side of the mean gestation length, indicating that not all insemination dates were recorded. Therefore, for the SLS data set in particular, using a non-return trait would have been

inappropriate, as cows inseminated just once in a lactation did not necessarily conceive to that insemination.

In progeny testing schemes it is useful to get information early. This can substantially reduce the time lag between making the test inseminations from a young bull and getting an initial prediction of breeding value, and therefore shorten male generation intervals. For example, information from incomplete lactation records can be used for routine genetic evaluations of milk production; the current requirement in the UK is a minimum of three tests (Animal Data Centre, 1996). Fertility traits could be evaluated in a similar way, as young sire evaluations of non-return traits would be available sooner than conception rate traits. However, as mentioned above, non-return traits have several pitfalls. If genetic correlations between maiden heifer and first lactation fertility are high, then it may be possible to use conception rates in maiden heifers as a selection criterion for fertility. However, at present many milk recording agencies record only information on lactating cows.

One of the aims of this thesis was to investigate the genetic control of various common measures of fertility. In addition to this some of the relative merits of the various fertility measures have been discussed here. At present it is difficult to determine which, if any, of the fertility measures would be an appropriate selection criterion in a breed improvement programme. Fertility scores seem to be the most useful as they achieve a desirable goal - fewer straws of semen per conception, although some adjustment should be made for length of lactation, i.e. conception rates may be better for cows inseminated later. However, incomplete insemination records would lead to biases in non-return rate traits (and conception rate traits to a lesser extent). Restriction of records to those with at least two consecutive calving dates also has limitations as it would mean that the least fertile cows would be excluded. An alternative would be to use correlated traits as selection criteria. Possible traits include those related to hormone profiles (e.g. Darwash *et al.*, 1997) and body tissue mobilisation such as condition score, liveweight changes over lactation (or at calving) and dry matter intake. Condition score is measured once in

first lactation heifers by the Holstein Friesian Society of Great Britain and Ireland (HFS), so a large scale analysis of the relationship between fertility and condition score should be possible.

6.4.2 Health

SLS record seven different health disorder codes (Table 2.1). A low incidence or ambiguity of recording category led to analysis of just three of the traits recorded: mastitis, lameness and milk fever. Mastitis and lameness are the most prevalent and economically important diseases in UK dairy cattle (Kossaibati and Esslemont, 1997), so these traits would be obvious choices in future breeding programmes. As failure to conceive was the main culling reason in DAISY recorded herds (Esslemont and Kossaibati, 1997), it would be useful to breed for improved reproductive performance. However, in the SLS analysis, the heritability of breeding problems was very low (unpublished results), presumably because this trait is ambiguously defined. So, if possible, a more objective indication of fertility problems should be used. In the DAISY recording scheme several fertility problems are recorded, for example retained placenta and vulval discharge (metritis) (Kossaibati and Esslemont, 1995). Unfortunately data on these traits were not available for this analysis, but should be included in future genetic analyses.

There are several problems associated with using data of clinical cases of disease for genetic improvement programmes:

i) Disease is generally considered to be an all-or-none trait; in reality there are degrees of severity and different people (recording on the same farm) may have different thresholds.

ii) If farmers are concerned about what the data they collect will be used for, they may differentiate between recording cases of disease within their herds, e.g. they may not record clinical cases of disease for high value stock.

iii) Collection of disease data may be sporadic in voluntary data recording schemes.

For these reasons correlated traits may be particularly useful as selection criteria for health disorders. Linear type scores and SCC were the only potential predictor traits considered in this study, as PTAs for these traits are already available in the UK. The estimate of the genetic correlation between clinical mastitis and SCC was 0.65 (Chapter 3). Although this analysis should be regarded as preliminary, as there were relatively few SCC records, it should encourage breeders that selection for low SCC will result in a reduction in mastitis. However, from the index calculations (Chapter 5) it appeared that in order to prevent a further deterioration in mastitis, a large weight would need to be assigned to SCC.

Regressions of health disorders on sire PTAs for type indicated that some type traits may be suitable future selection criteria (Chapter 3). A limitation of this approach may have been that sire PTAs do not relate particularly well to daughter conformation in small data sets. An alternative and perhaps better approach would have been to estimate correlations between health and linear type scores of the females, but there were insufficient pedigree females in the DAISY data set to do this analysis.

There may be particular problems associated with recording lameness consistently and accurately, particularly as there are many types of lameness and subclinical cases are not easy to identify accurately. While adjustment for herd-year-season effects are important in this respect, using correlated traits may be particularly useful. McDaniel (1995) and Boelling (1997) suggested that selecting for hoof characteristics and locomotion may be effective as strategies to improve resistance to lameness.

Correlated traits, rather than direct evaluations, may be useful as selection criteria for health disorders. However, if health and fertility traits are measured in future progeny testing schemes, then direct evaluations will usually be of greater value than predictor traits when progeny group sizes are large (a possible exception to this is lameness). For example, results from Chapter 5 showed that information on SCC was redundant when mastitis was recorded. Philipsson *et al.* (1994) suggested that SCC

may be useful in conjunction with information on mastitis when progeny group sizes are small. In the UK, SLS and DAISY are the only schemes to record production, health and fertility information. Together these schemes account for less than 10% of UK dairy cows and, even then, not all participants of the scheme record health and fertility events. So for the time being, identifying predictor traits which can be evaluated for progeny testing schemes is particularly important. Without question, data recorded by SLS and DAISY will be extremely valuable to enable relationships between predictor traits and health to be investigated.

6.5 International evaluations

Dairy cattle breeding has become an international business over the past few decades. Exchange of semen and embryos between countries has allowed breeders in one country to make use of genetic evaluations in other countries. Much of this work has been supervised by the International Bull Evaluation Service (INTERBULL). In the past, international proofs were estimated using international conversion formulae and these were available for only production traits. Conversion formulae are based on sires' proofs in two countries - the foreign and importing country. One of the main limitations with conversion formulae is that the sires rank the same in different countries and so they do not account for genotype by environment interactions. Conversion formulae have now been superseded by a relatively recent technique, known as Multiple-trait Across Country Evaluation, or MACE. MACE treats records on the same trait from different countries as if they were different traits. This allows for differences among heritability of the trait of interest and allows for different correlations between this trait recorded in different countries. Thus sires rankings can differ among countries.

In the future, MACE evaluations for health and fertility traits may be feasible. Countries can decide whether to record and evaluate health and fertility themselves, or rely on MACE procedures that use information from correlated traits (e.g. linear type scores and SCC) and information on relatives that have breeding values for health and fertility, such as in Denmark, Finland, Norway and Sweden. To do this

models for multi-trait as well as multi-country evaluations would be needed. For example, to obtain international evaluations for mastitis, information on clinical mastitis, SCC and possibly some type traits from Scandinavia could be combined with SCC and type traits from other countries (Rogers *et al.,* 1996). An advantage with MACE evaluations is that the best animals can be identified, for a range of traits (e.g. production, type, health and fertility) regardless of country of origin and as breeding goals differ between countries, bulls can be selected to match production circumstances.

Unless more herds record health and fertility, indirect proofs will probably be estimated for the UK. It would, however, be prudent to estimate genetic correlations between disease recorded in the UK and Scandinavian data to ensure that they are similar traits, as, for example, major mastitis-causing pathogens may differ between countries. Correlations between sire PTAs for health disorders recorded in different countries would be useful to see if there are genotype by environment (country) interactions for these traits in addition to differences in trait definition. For countries such as the UK, where there are a limited amount of health data, producing reliable sire PTAs would be difficult at this stage. However regressions of actual health records on sire PTAs for health (from Scandinavia) may be informative. If the results are favourable, this should help encourage the development of MACE procedures for health traits.

6.6 Further research

One of the main strengths of the data used in this study is that they came from three recording schemes with different levels of recording detail, the simplest being that of SLS and the most comprehensive, the Langhill data. Provided there are good genetic links between data sources (i.e. common sires), correlations between traits recorded in different data sets could be estimated. For example, information on dry matter intake, changes in condition score and liveweight are available for Langhill animals only, while data on health and fertility traits are available for all three data sets. Additional information on traits can be obtained from other sources, e.g. condition

score and linear type scores from HFS. Variance components for different combinations of traits from different sources can be estimated using REML procedures which allow for unequal design matrices and missing observations (e.g. VCE; Groeneveld, 1996).

Using this approach, correlations can be estimated between traits currently recorded in smaller data sets, such as dry matter intake or changes in condition score over lactation, with traits available in larger data sets e.g. health and fertility traits. This type of scenario would be of particular use to investigate the role of body tissue mobilisation. Another use of this approach would be to help identify potential predictor traits for health and fertility traits. As long as only a small proportion of herds have health records, future research should prioritise investigations of traits which may be used as alternative selection criteria. Most emphasis should be placed on investigating the relationship between health disorders and SCC and linear type scores.

Although parameter estimates were similar between SLS and DAISY, correlations between traits in the two data sets would have been more informative. However, because the data sets covered different time periods, there were relatively few genetic ties. As data continues to accumulate, more reliable parameter estimates of correlations between the two data sets will be obtained. Accessing data from other UK recording agencies may offer further opportunities to improve parameter estimates. NMR already collect service and calving dates and as they record 87% of UK dairy cows, use of these data would substantially increase the number of records available. Although SLS and DAISY are currently the only UK schemes to record health disorders, the results from this thesis may persuade other recording agencies to record health data.

There is still some way to go before routine genetic evaluations of health and fertility traits are available in the UK. At present, MACE evaluations based on information from correlated traits and relatives with health records from Scandinavian countries,

seem the most likely way this will be achieved. The next challenge is to incorporate these traits into a selection index, which would require economic weights for health and fertility traits. Deriving economic values for these traits will be even more complicated, if consideration is given to welfare and social issues. It is important that the negative consequences of selection for milk production are addressed. Correlations between production and health and fertility traits are unfavourable and most are relatively large. An index based on derived economic weights for traits in the breeding goal is still expected to lead to a decline in levels of health and fertility. The industry has to decide whether this is acceptable in the light of strong public opinion for animal welfare practices.

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